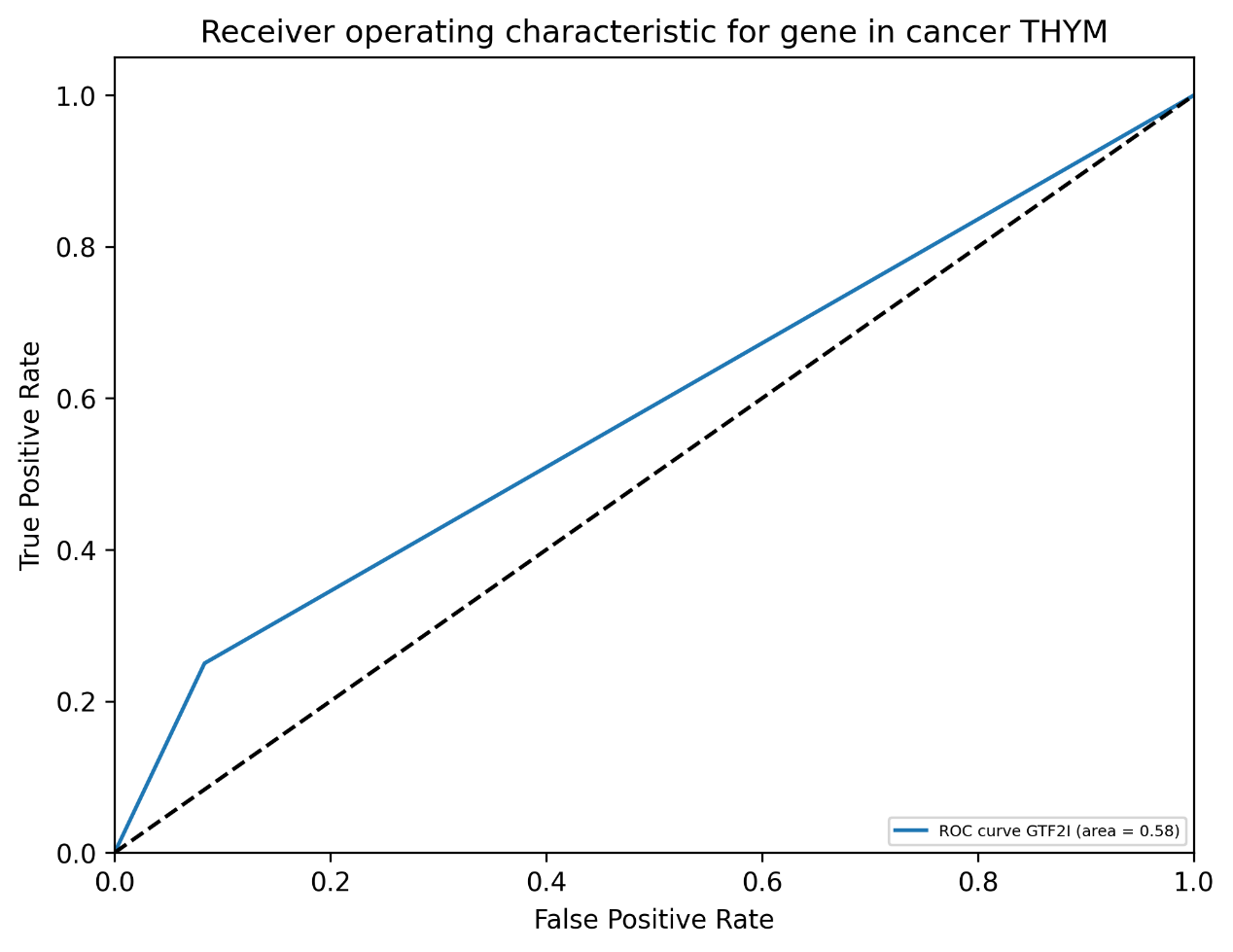
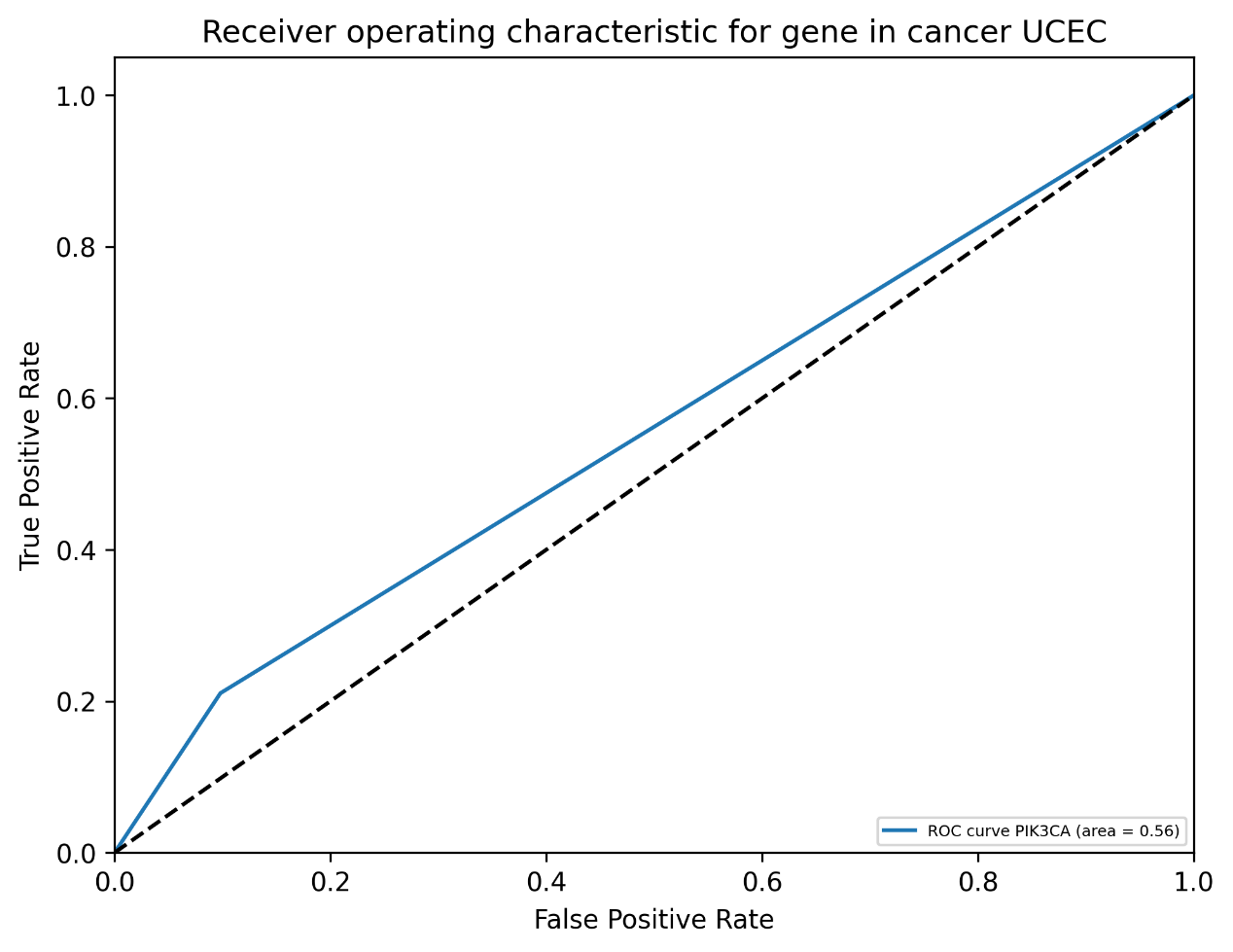
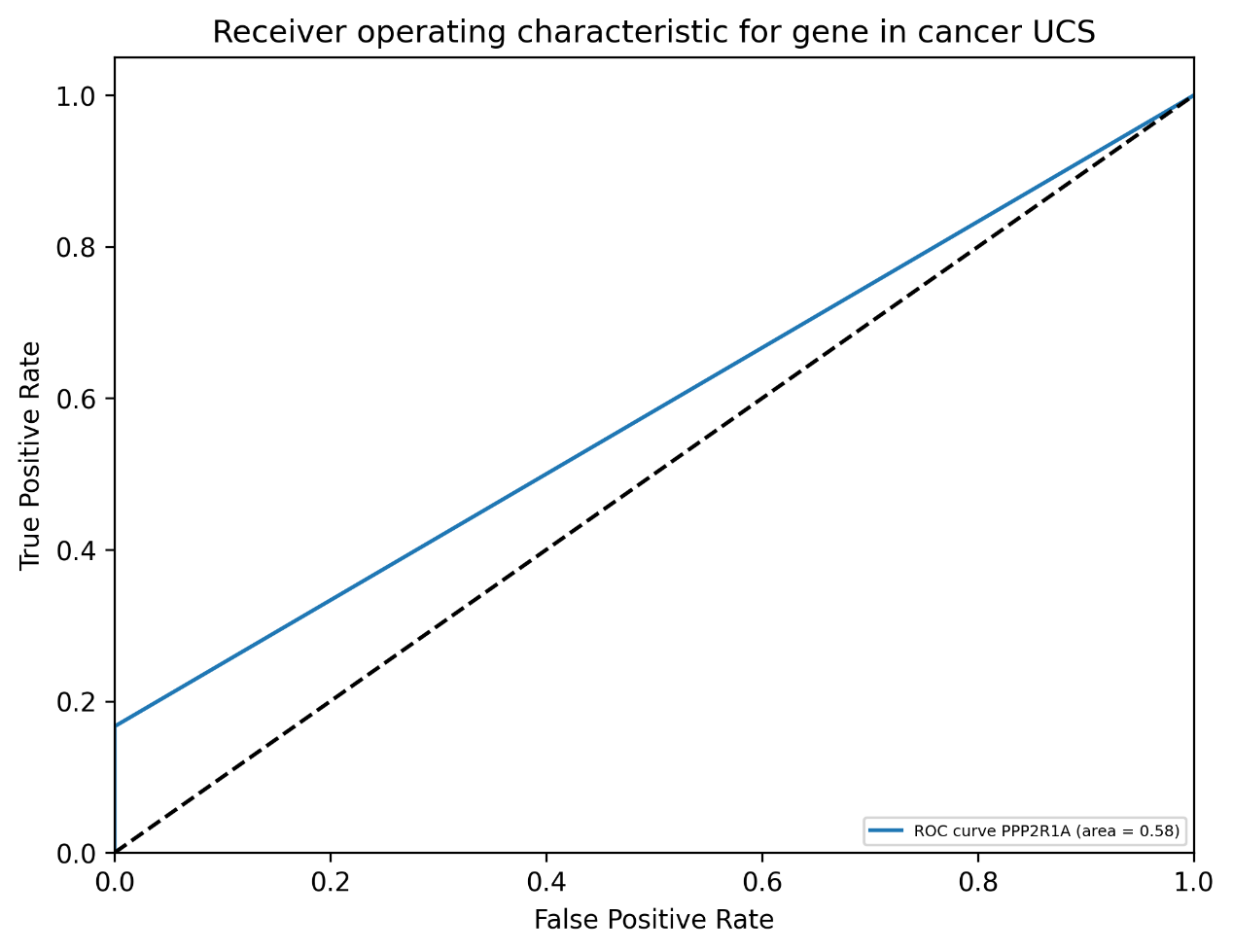
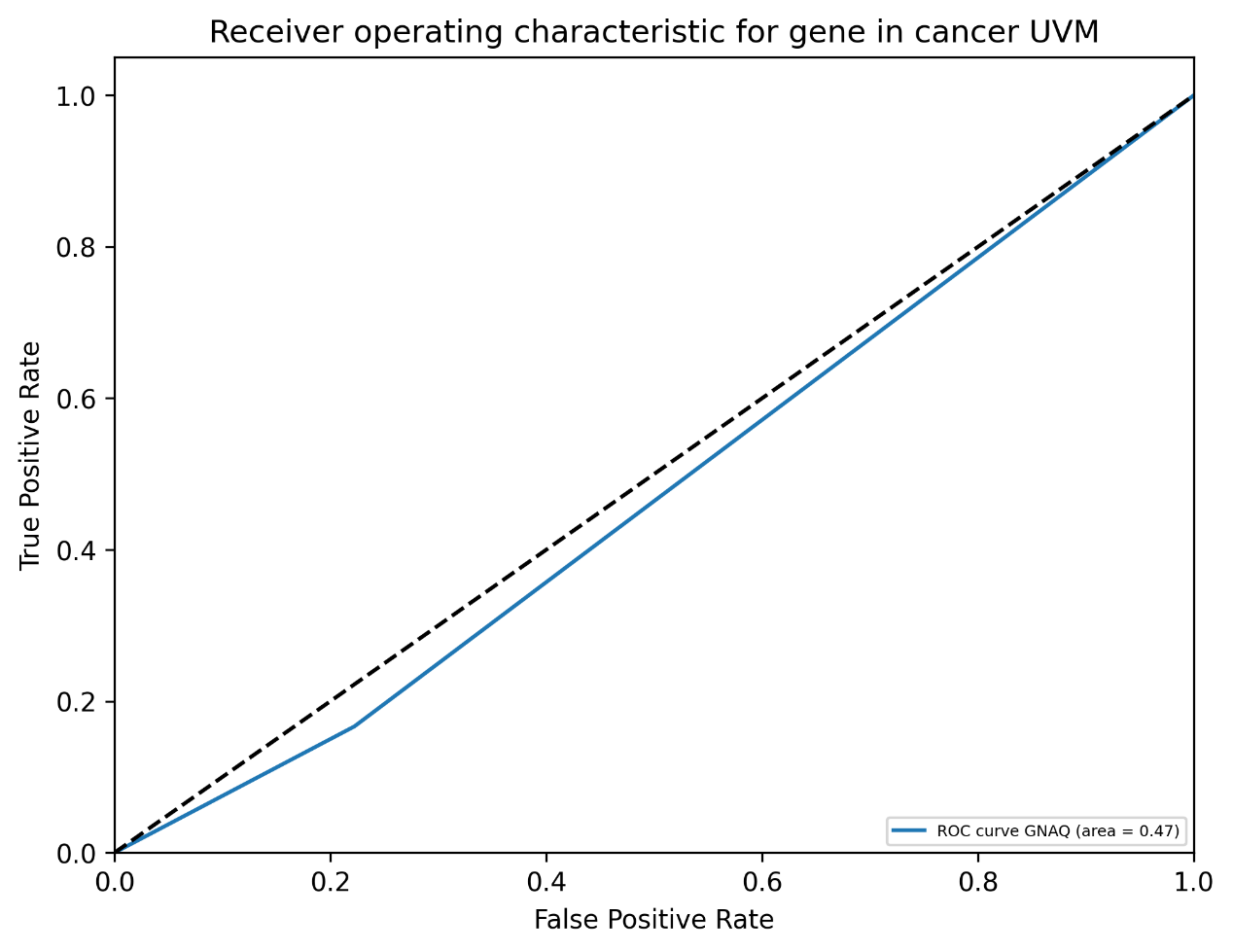
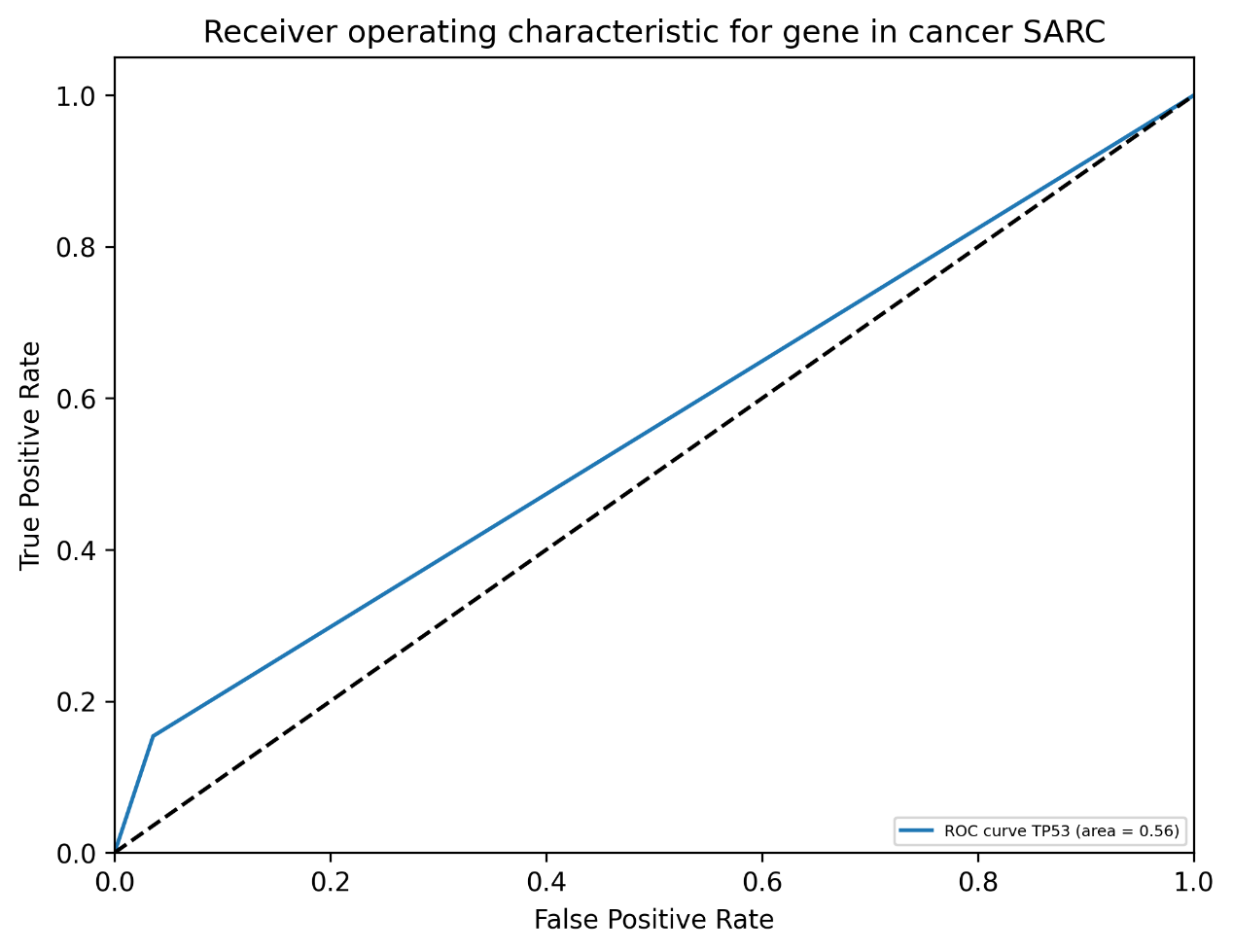
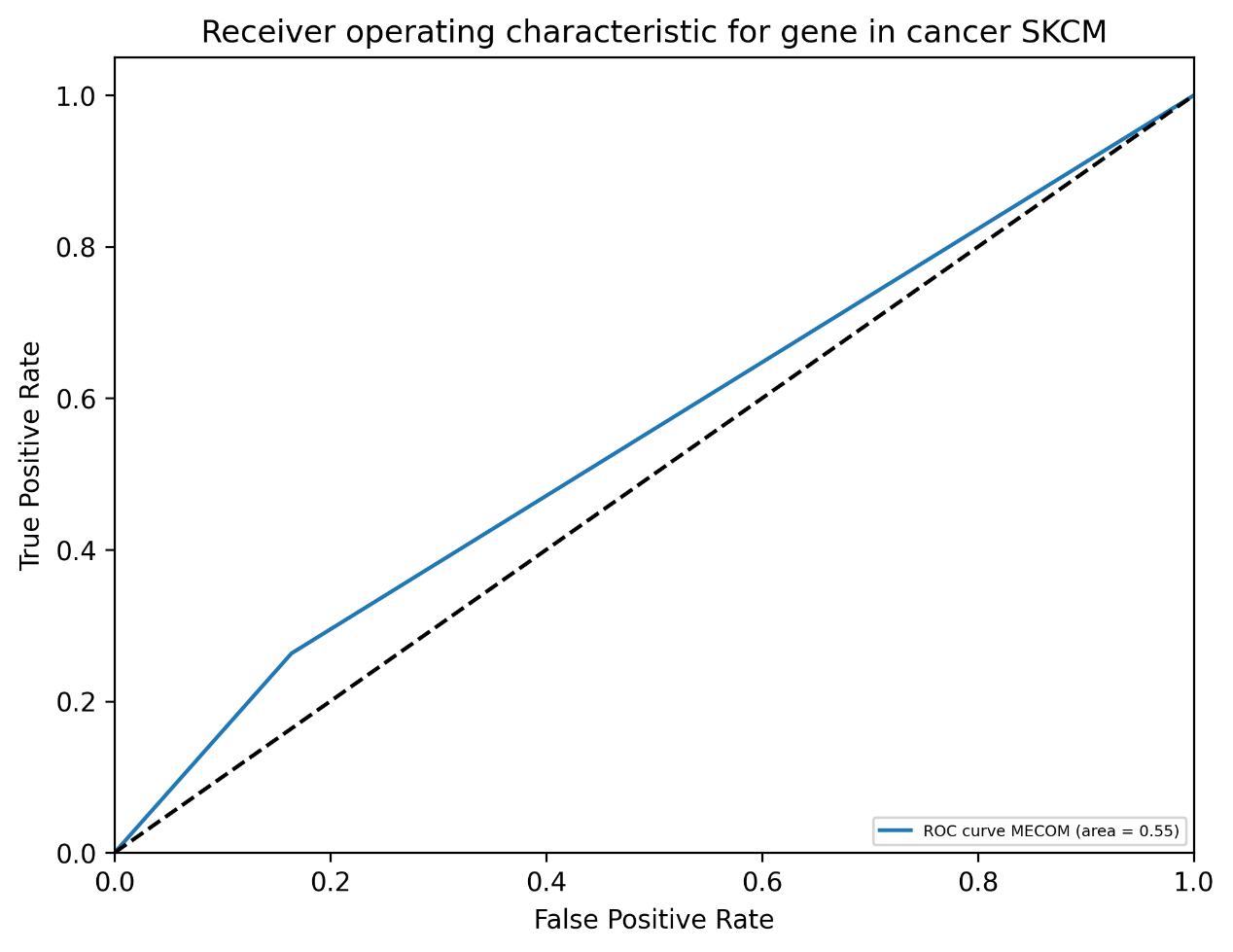
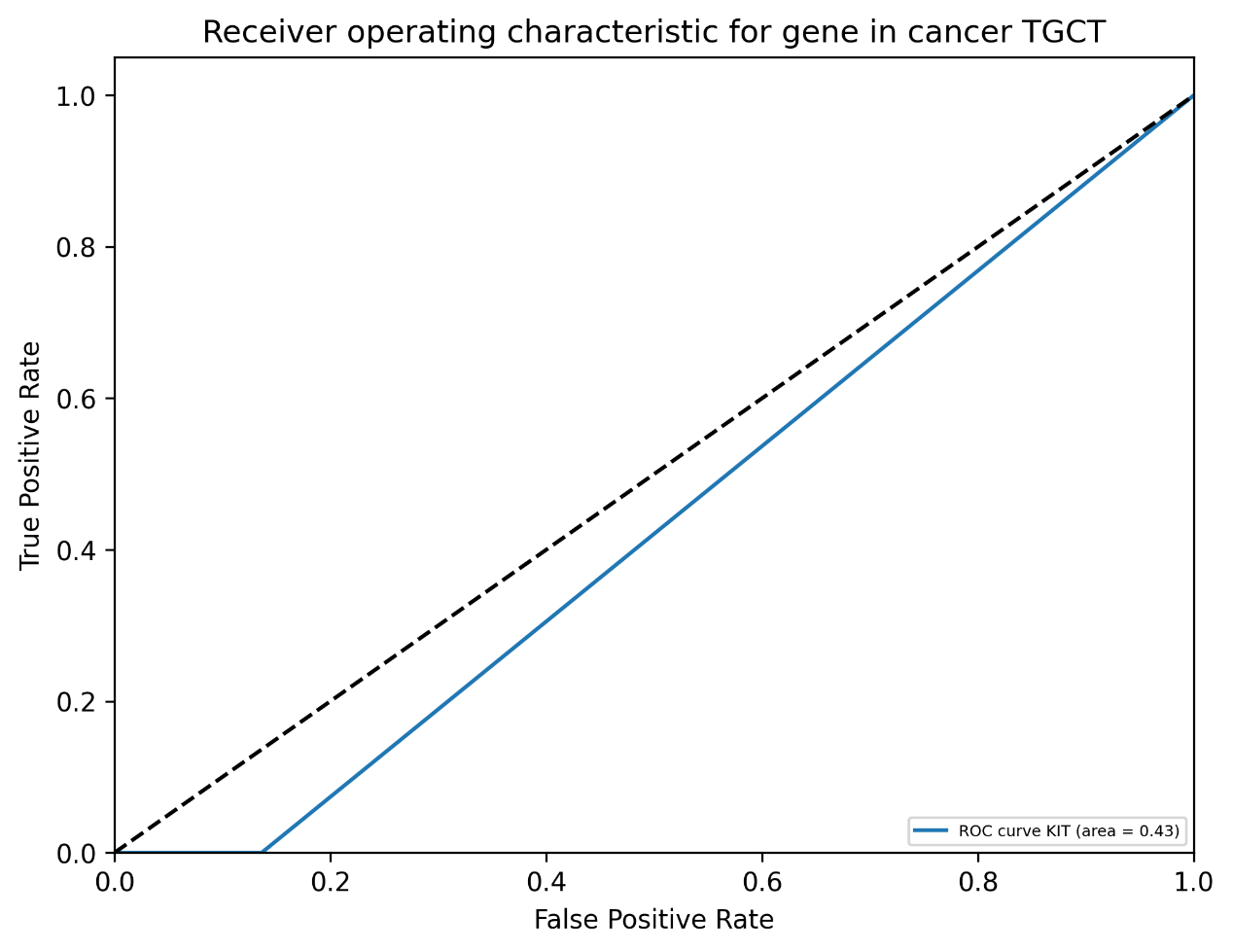
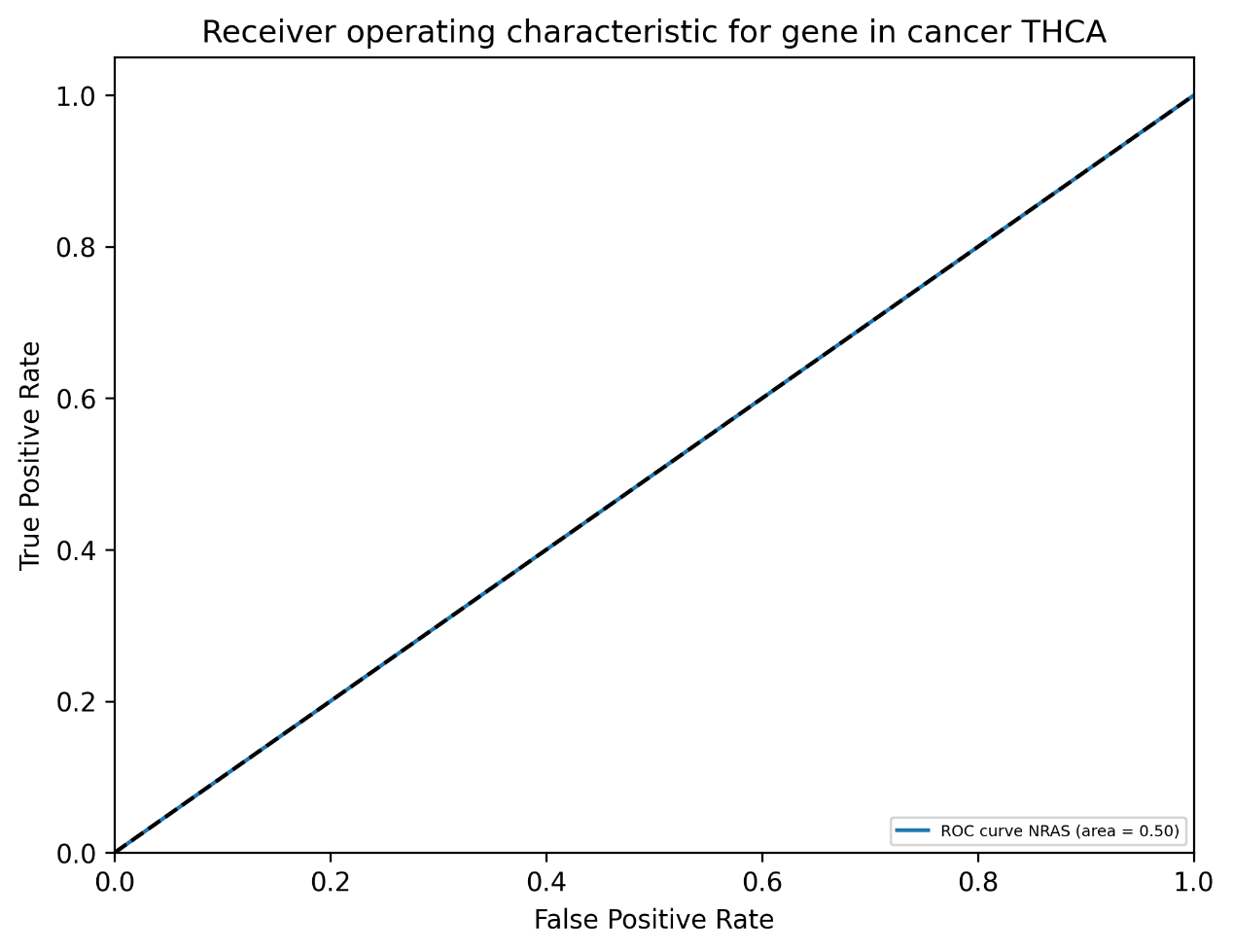
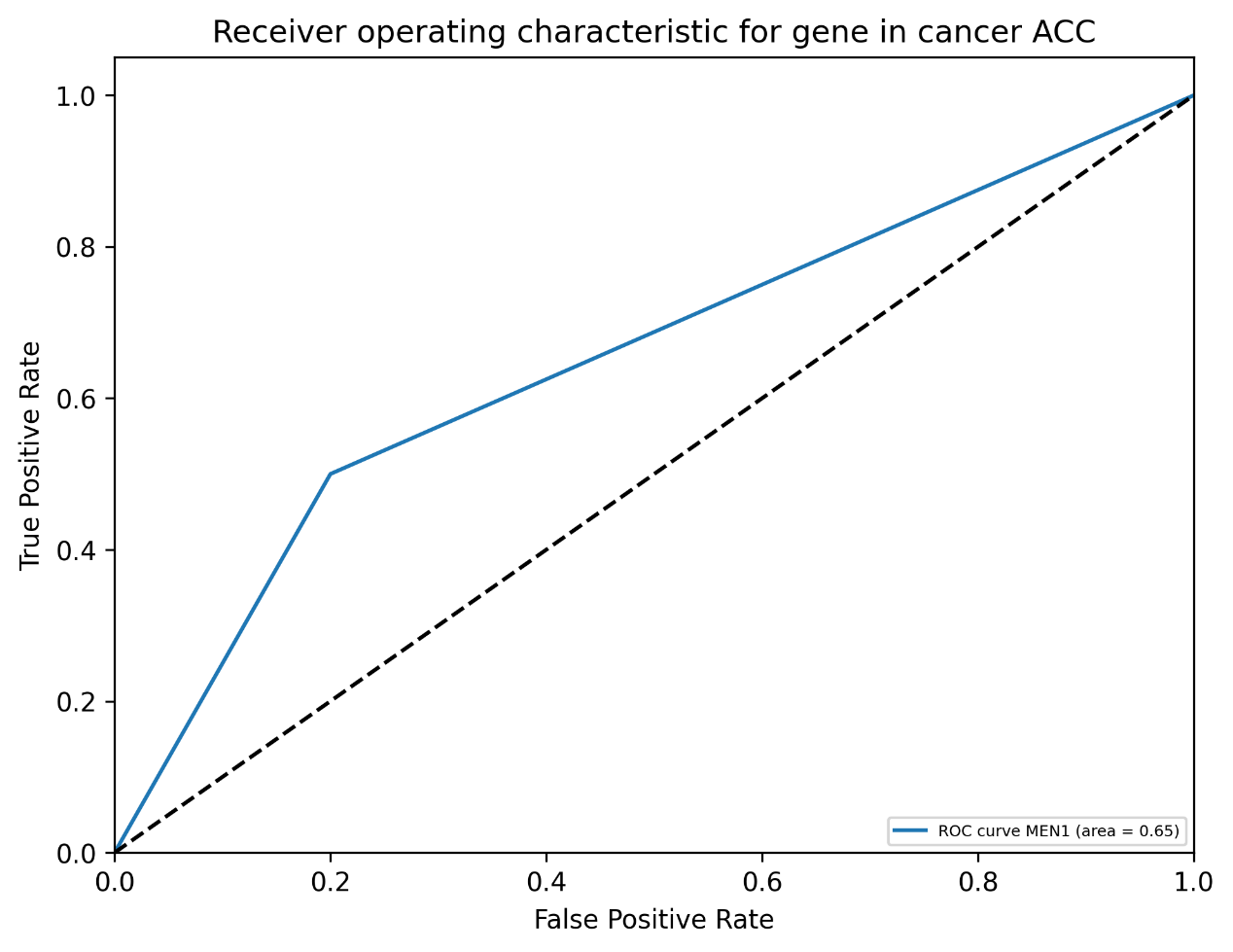
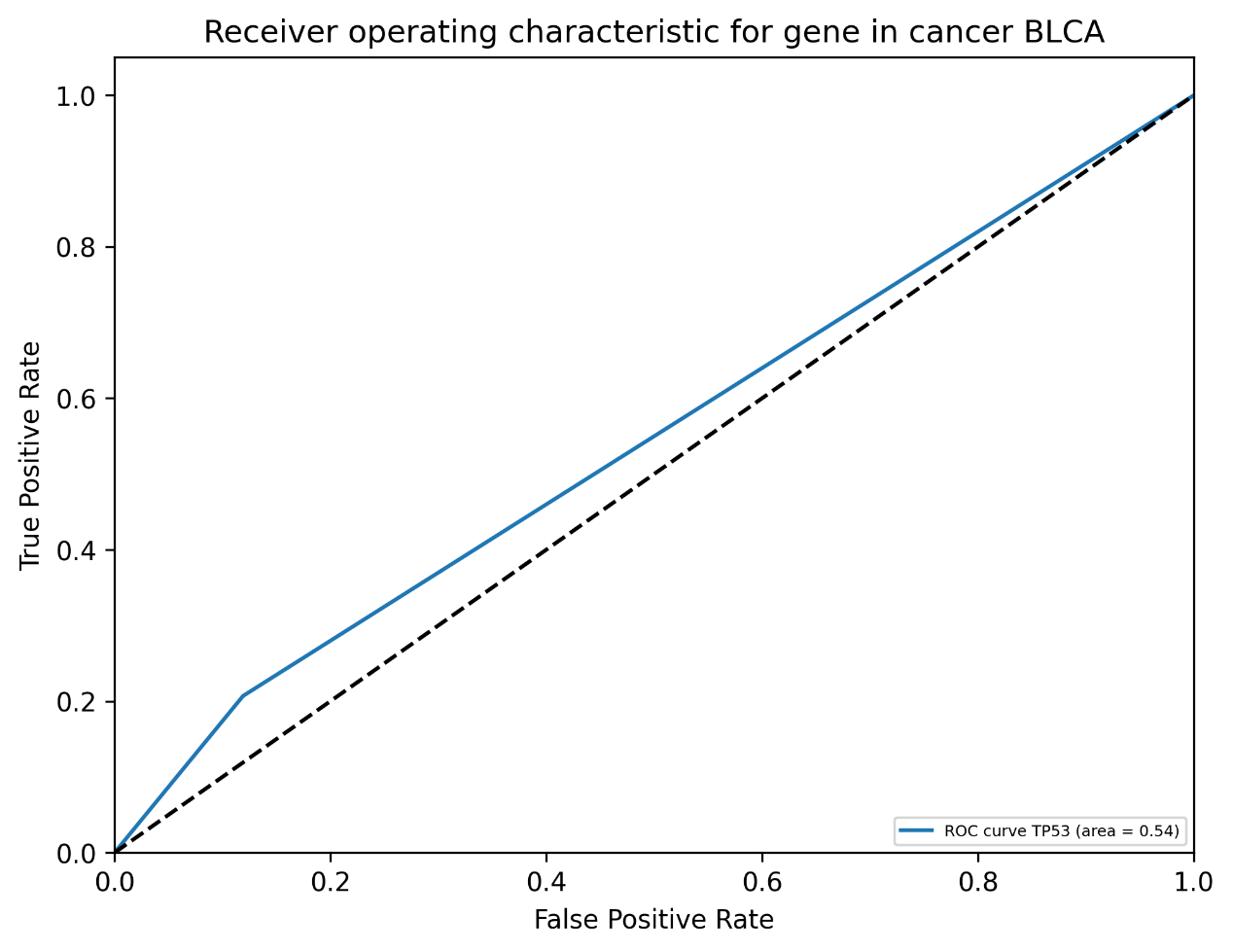
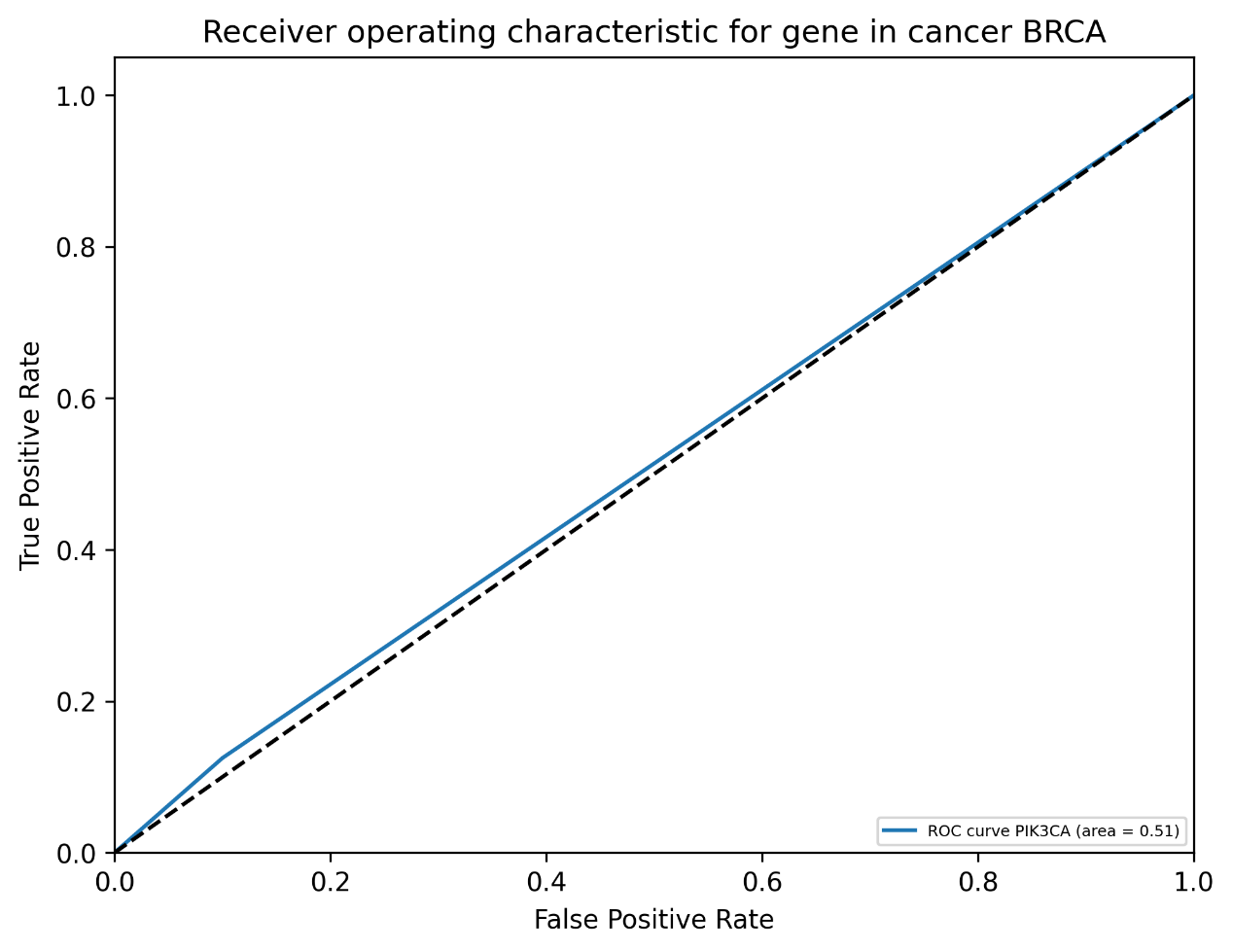
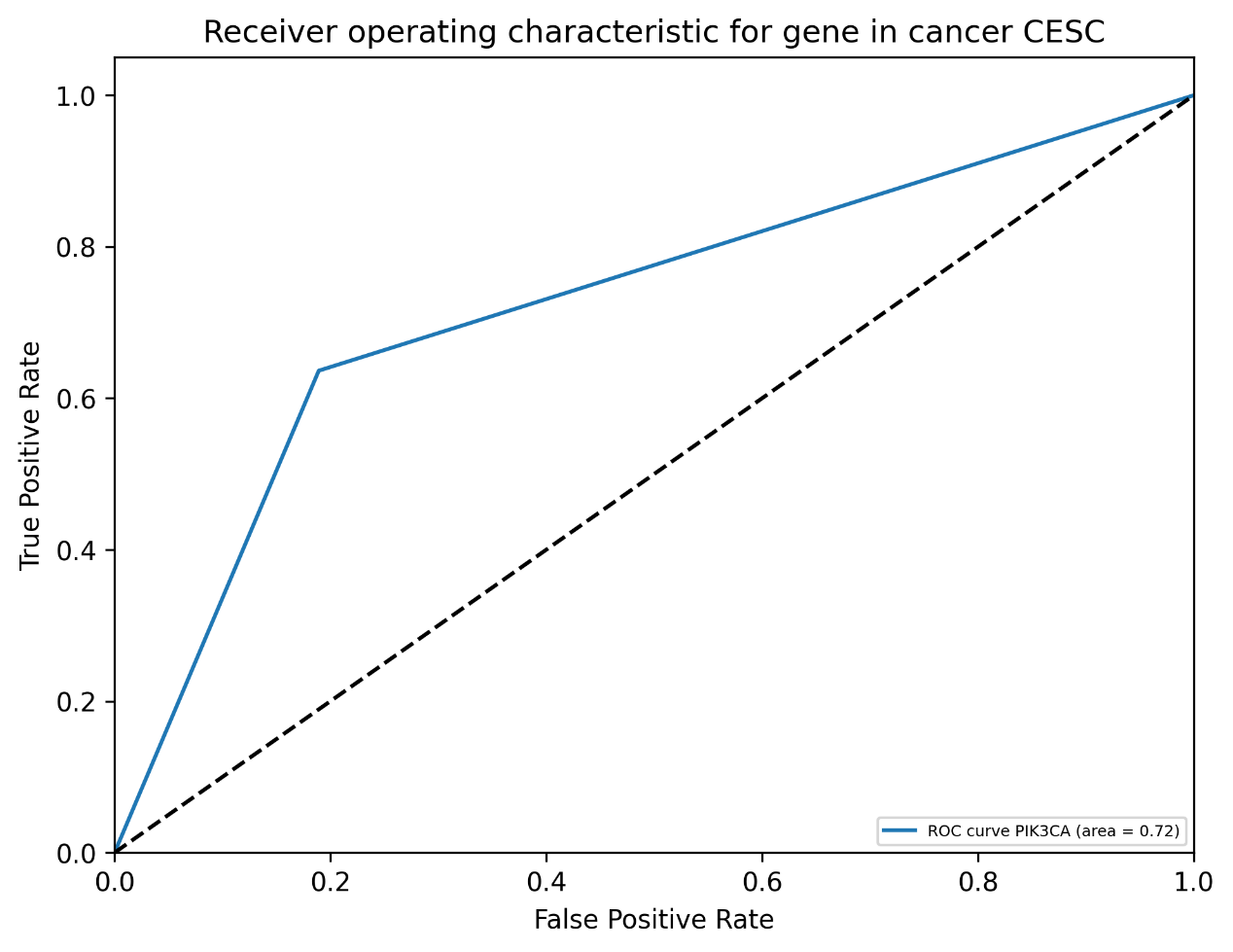
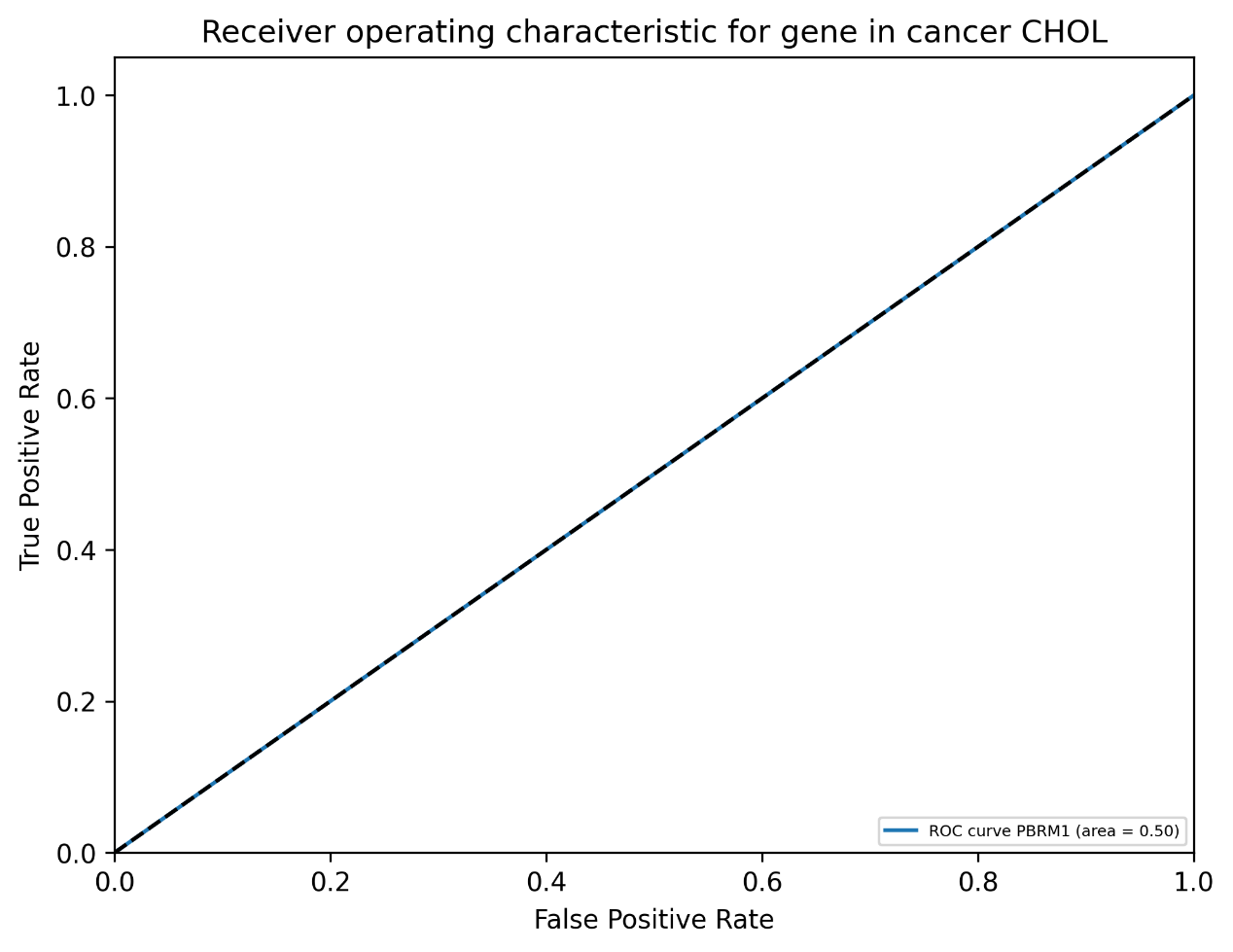
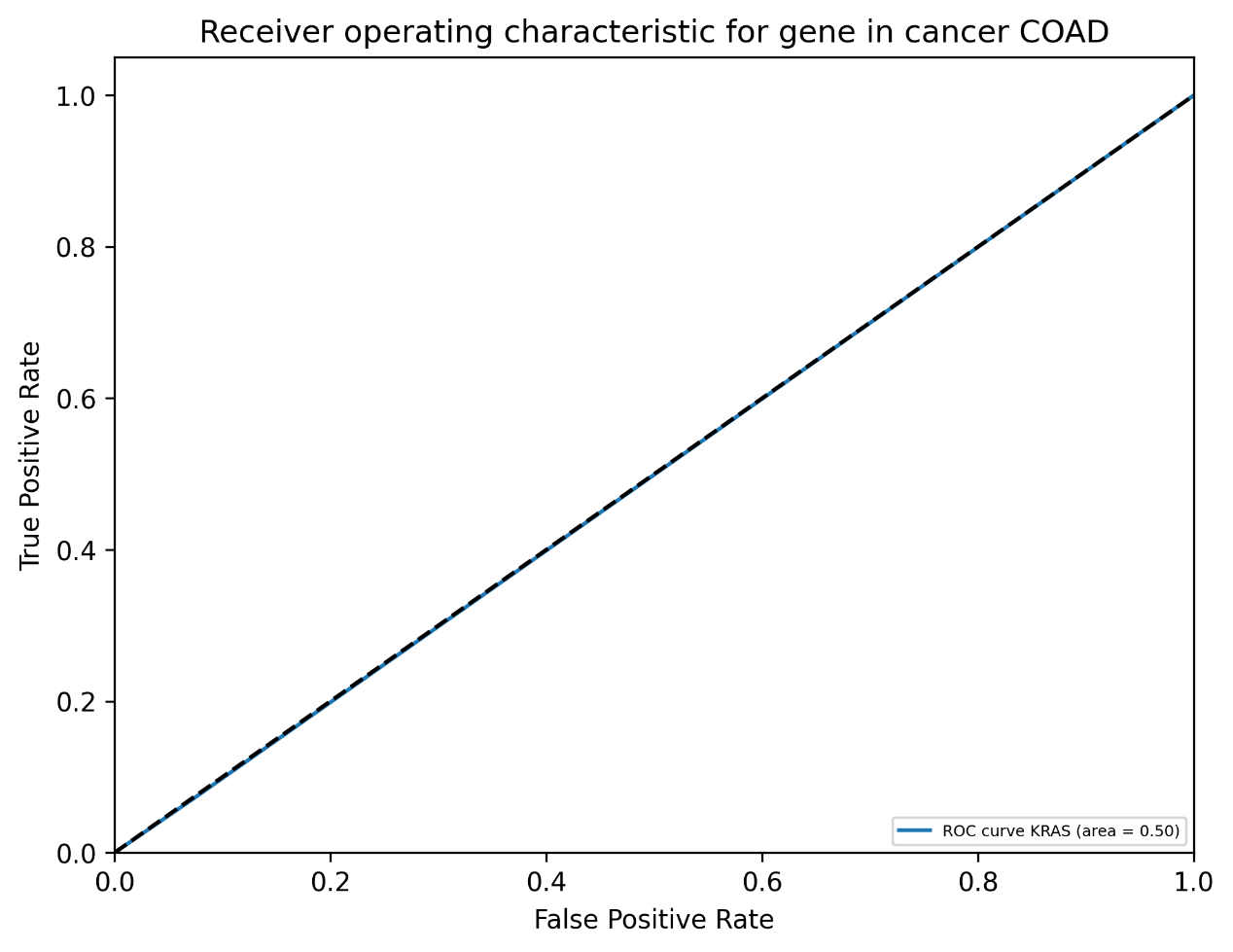
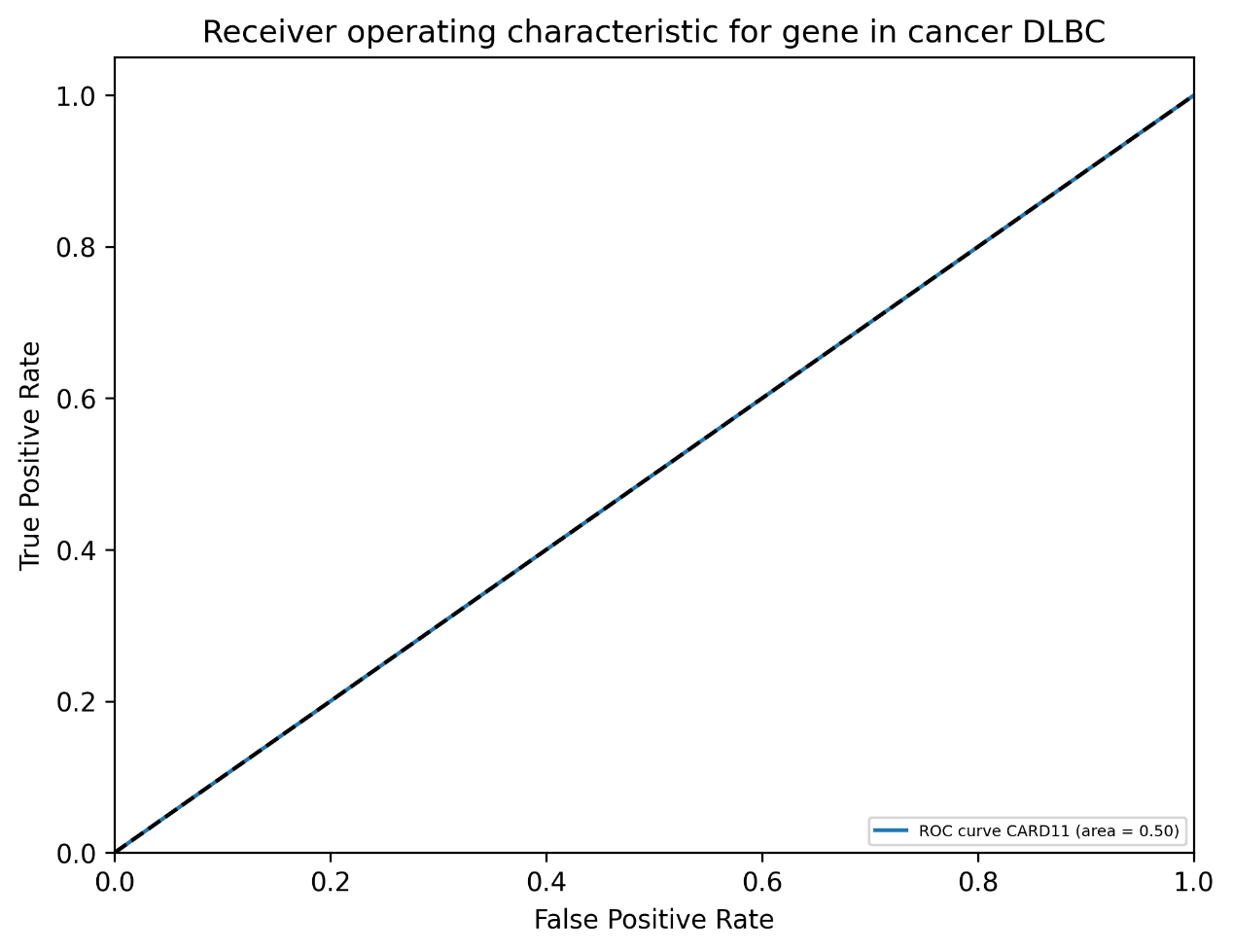
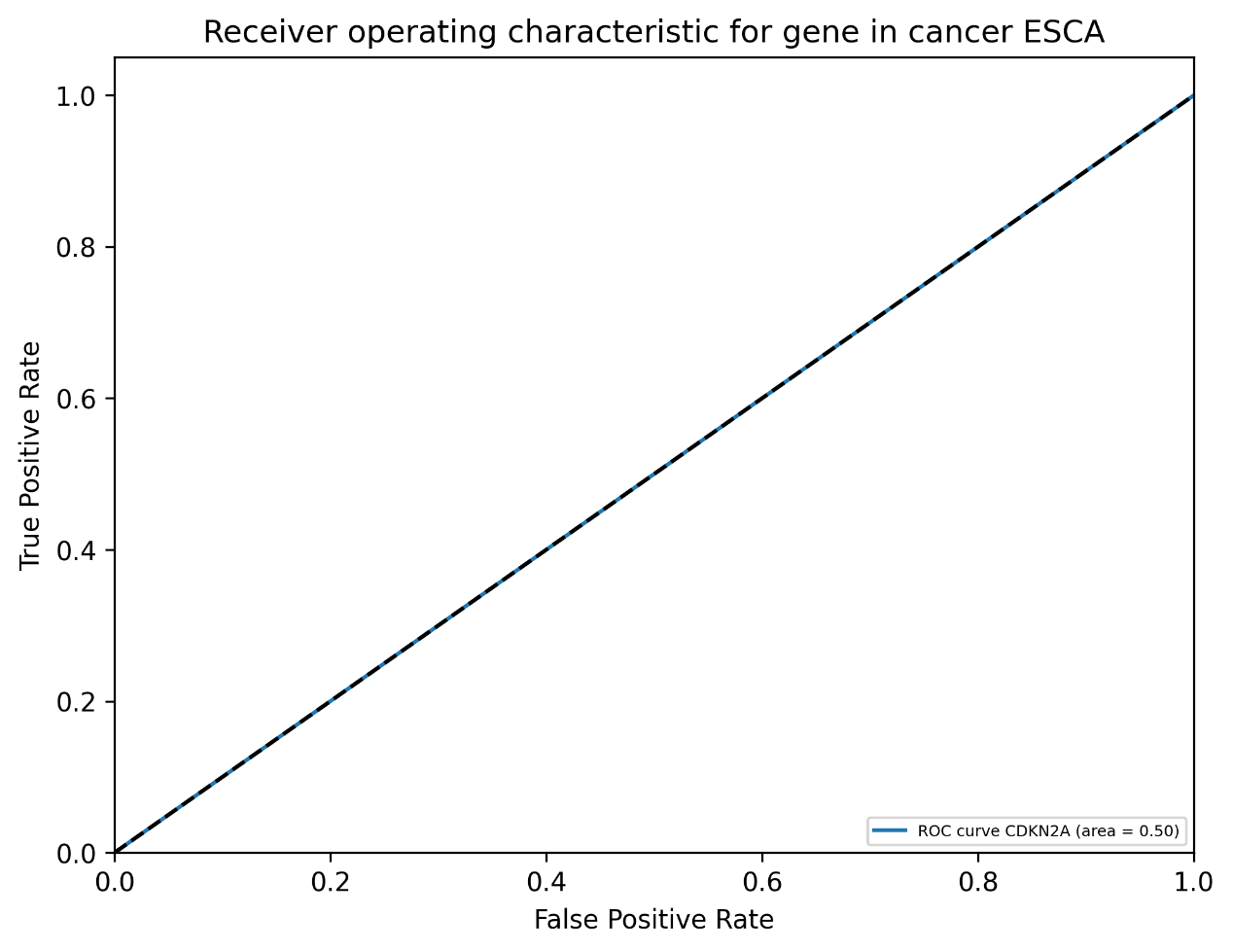
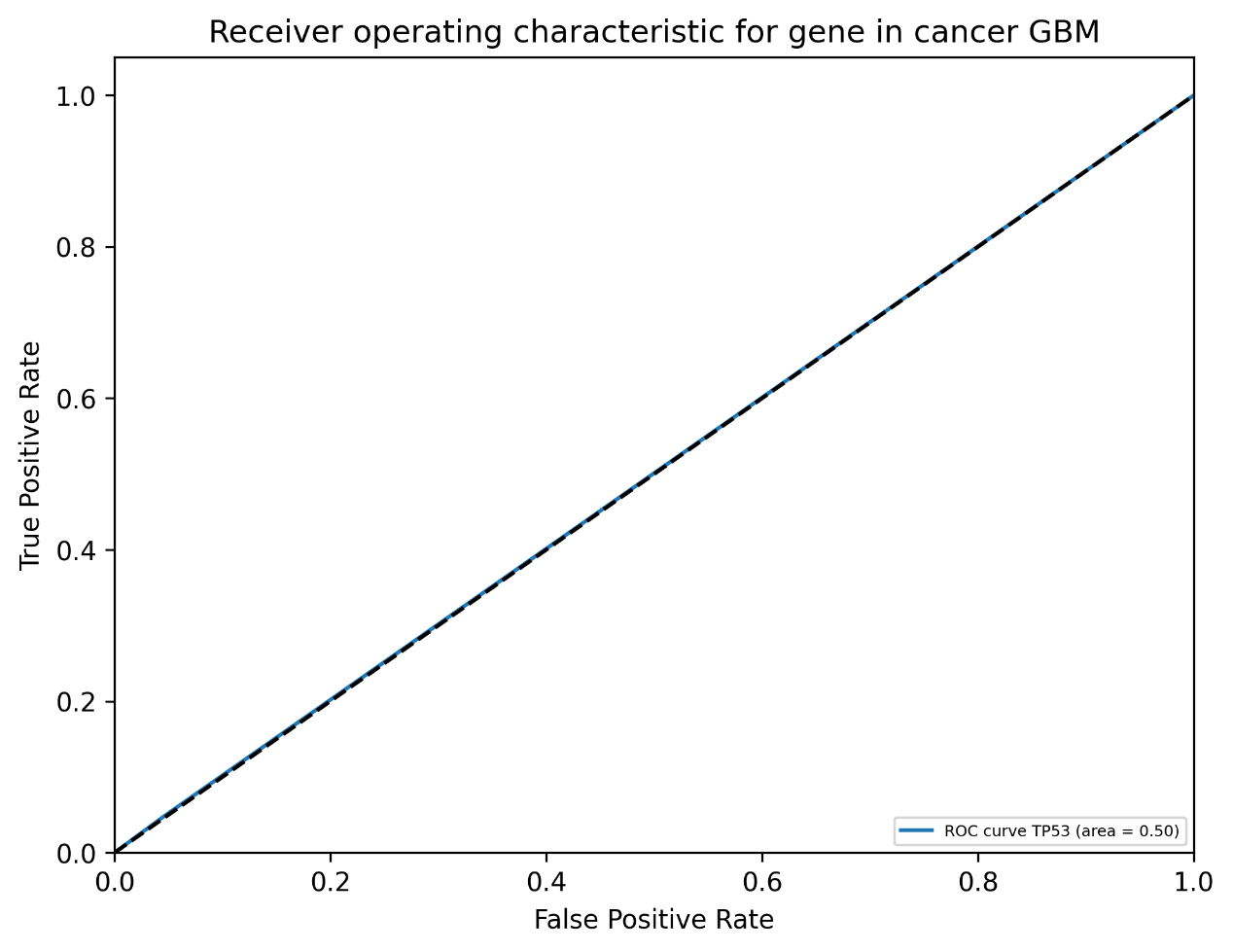
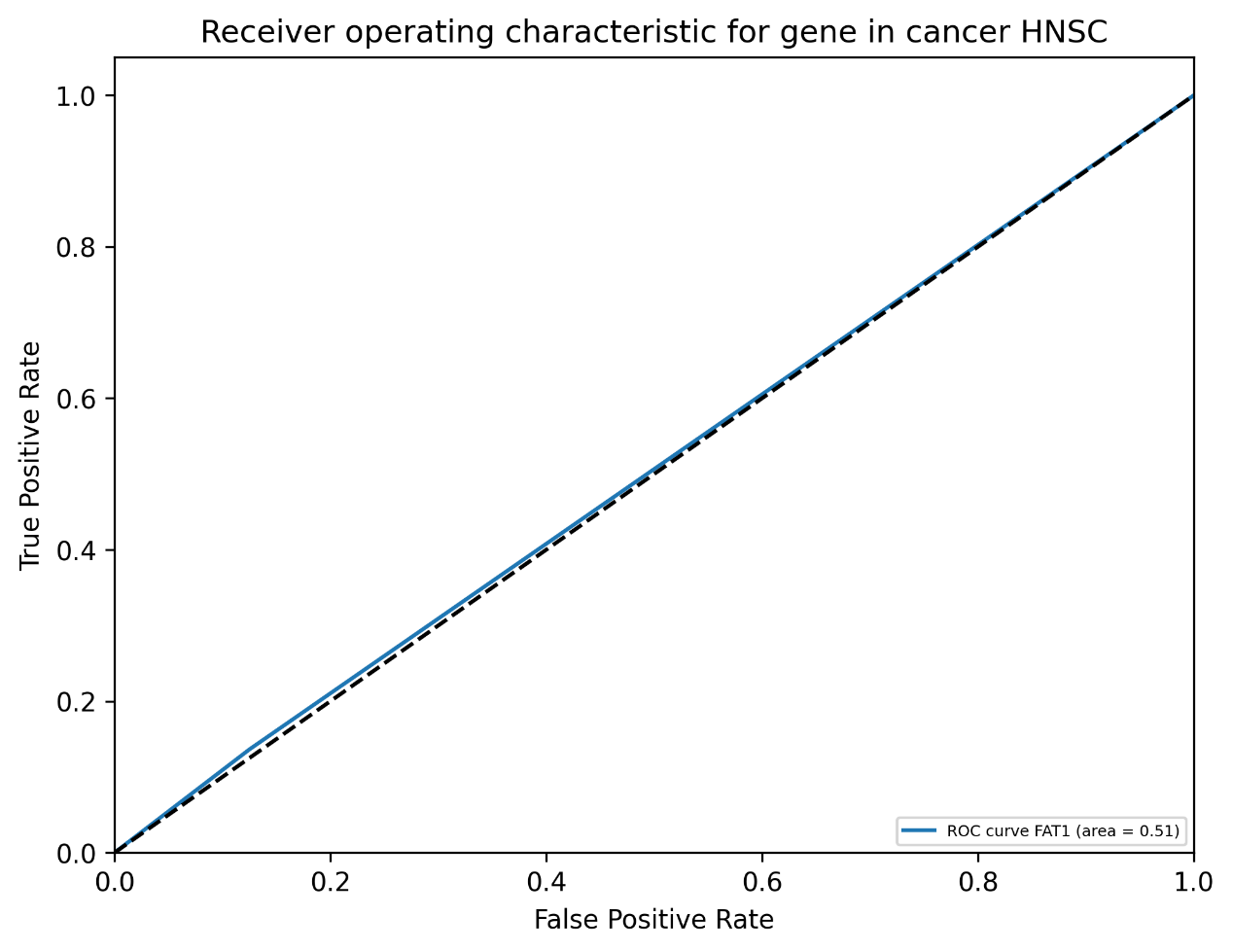
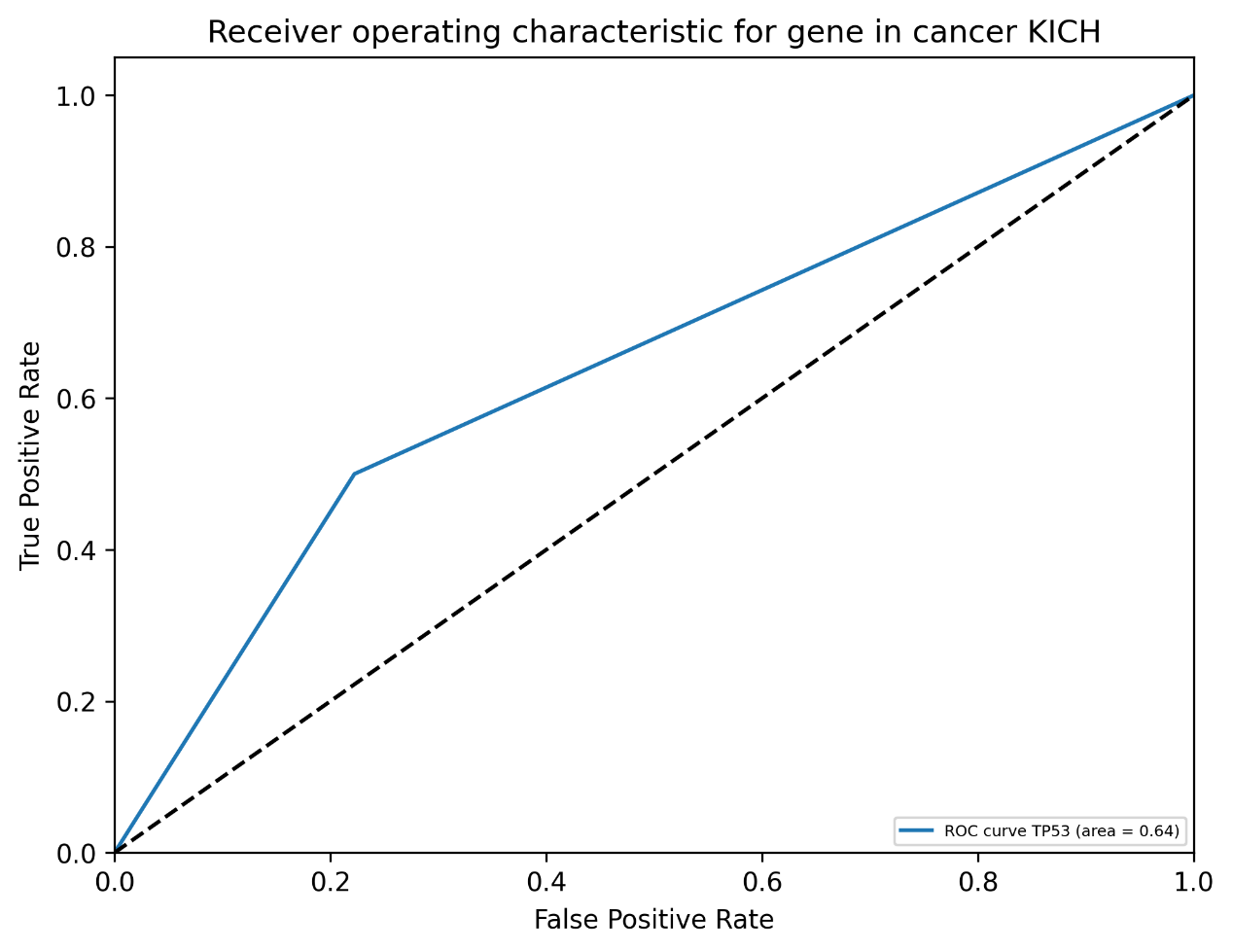
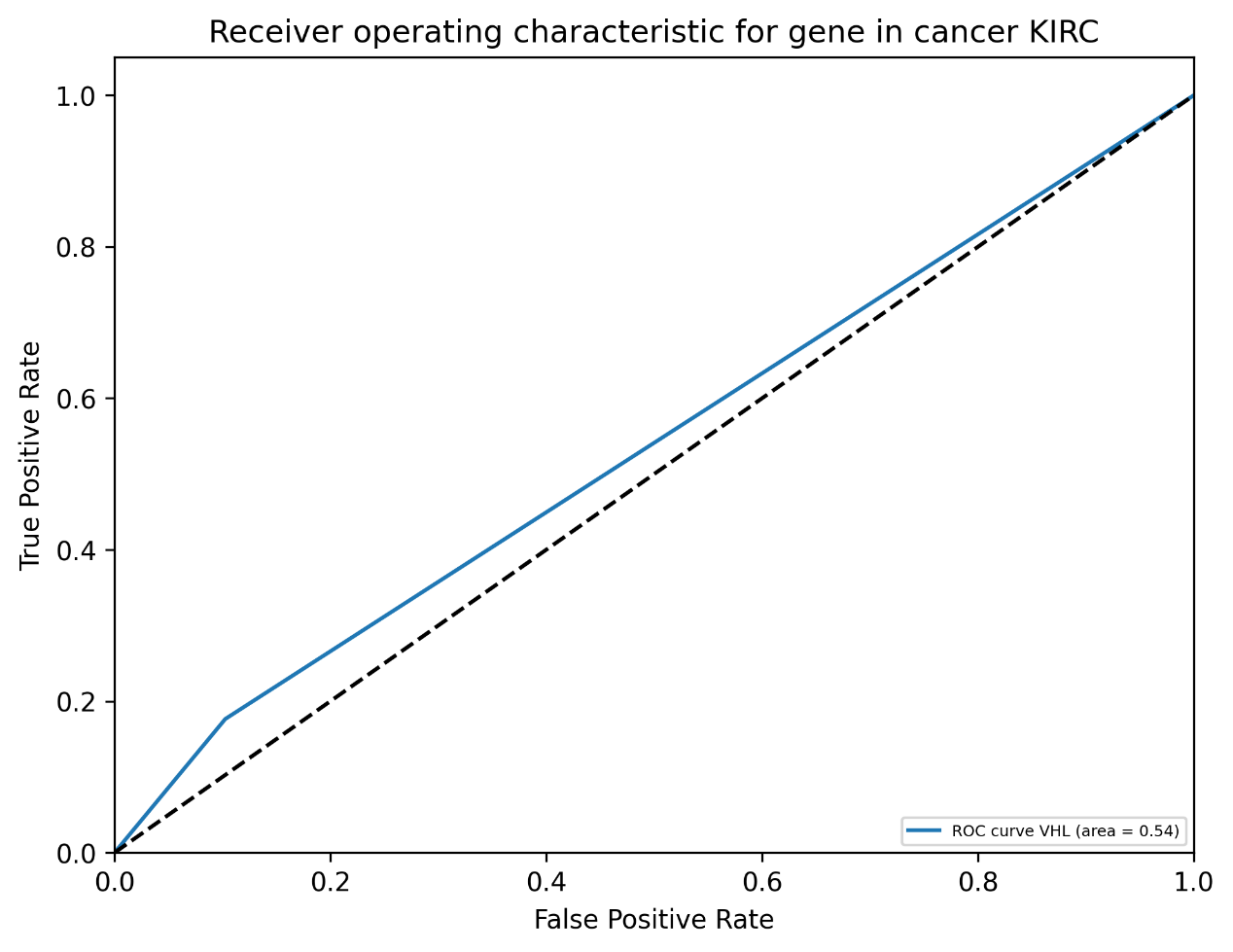
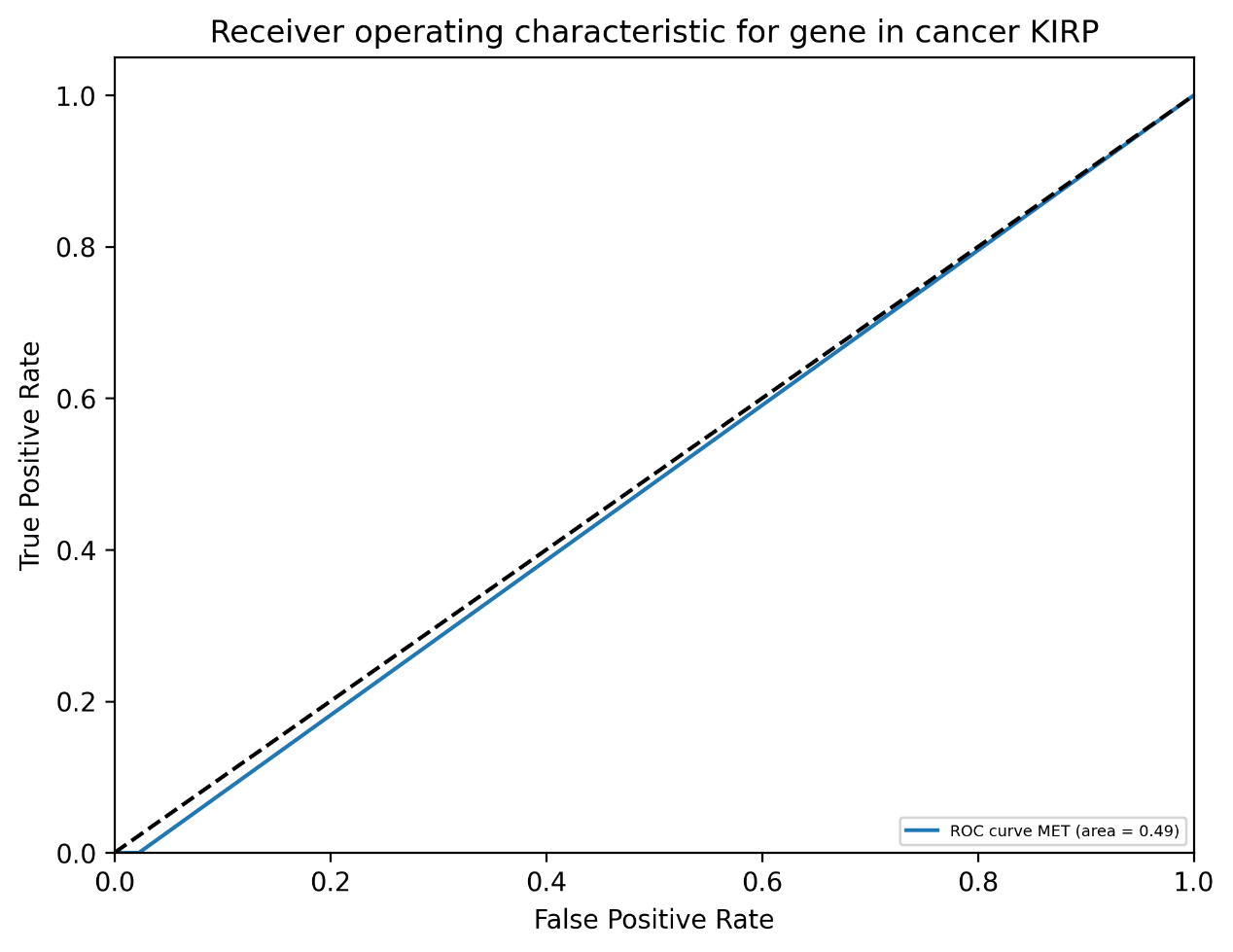
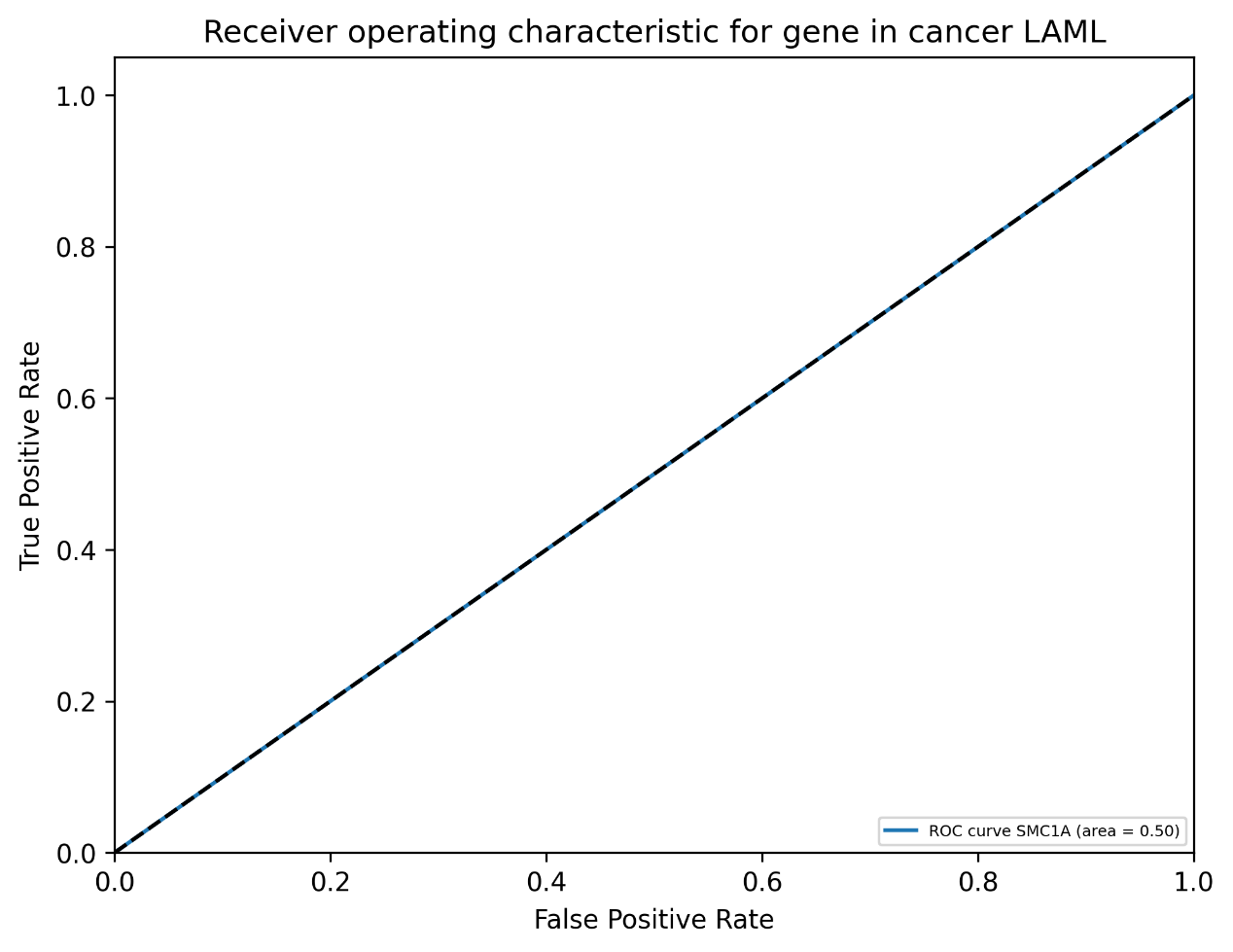
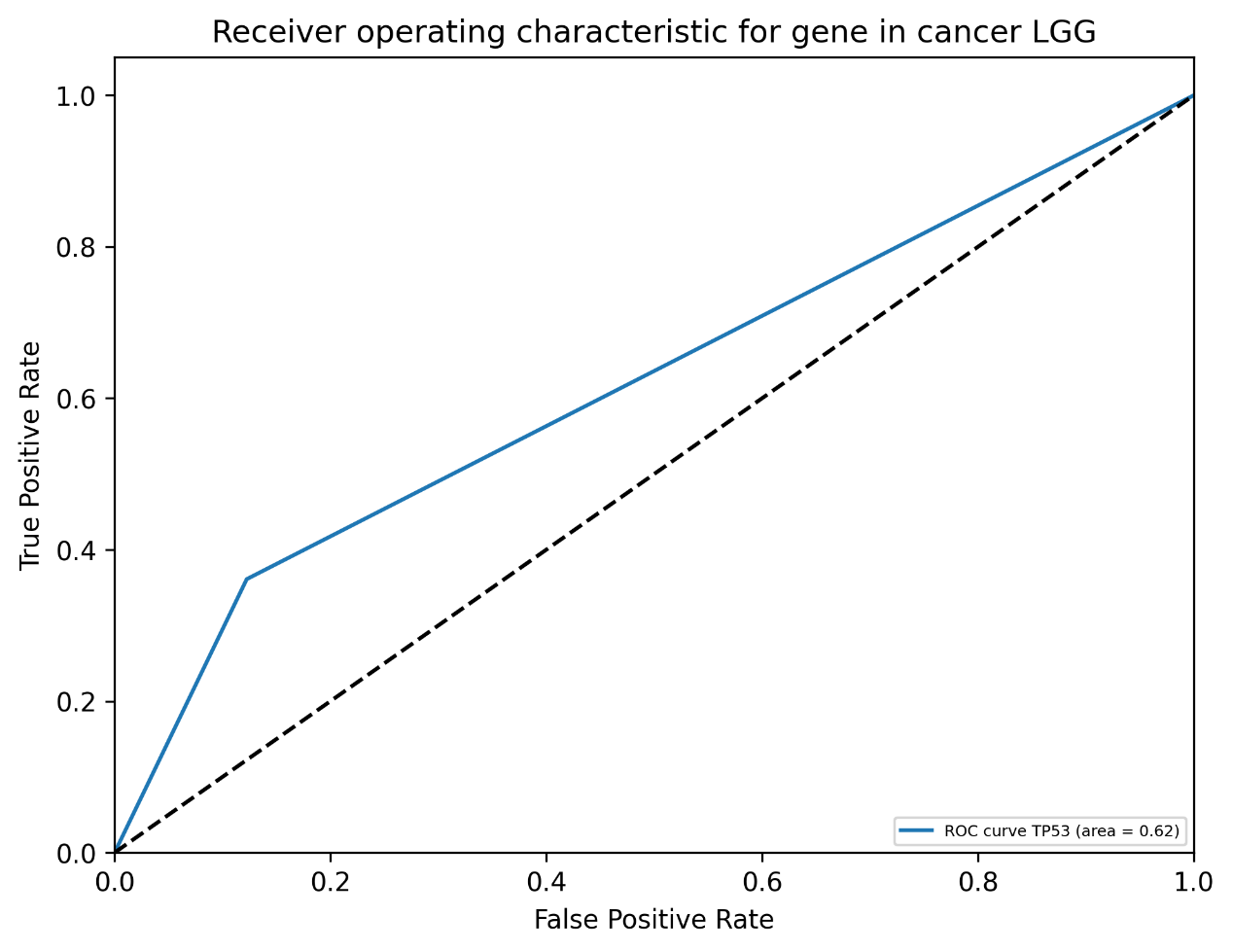
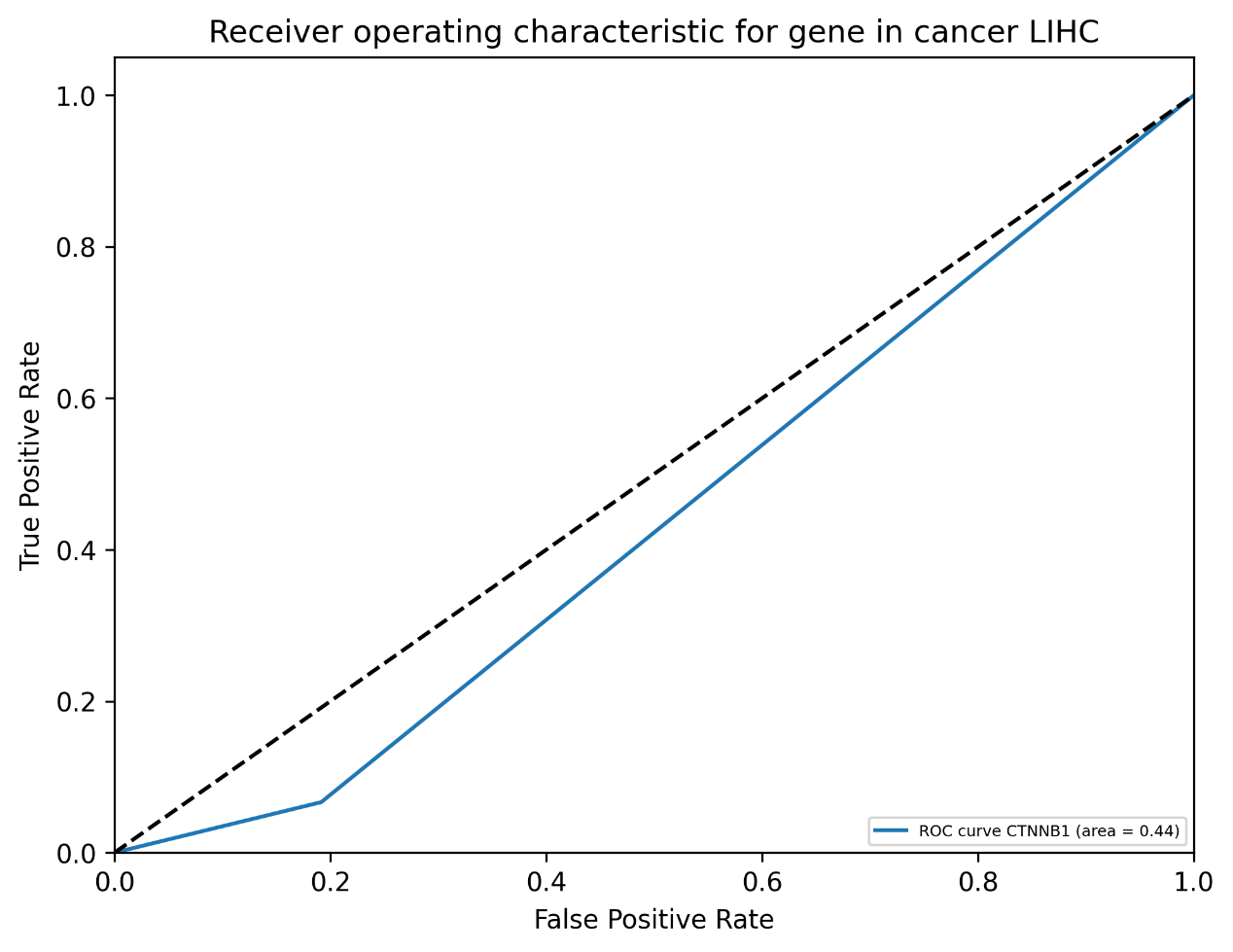
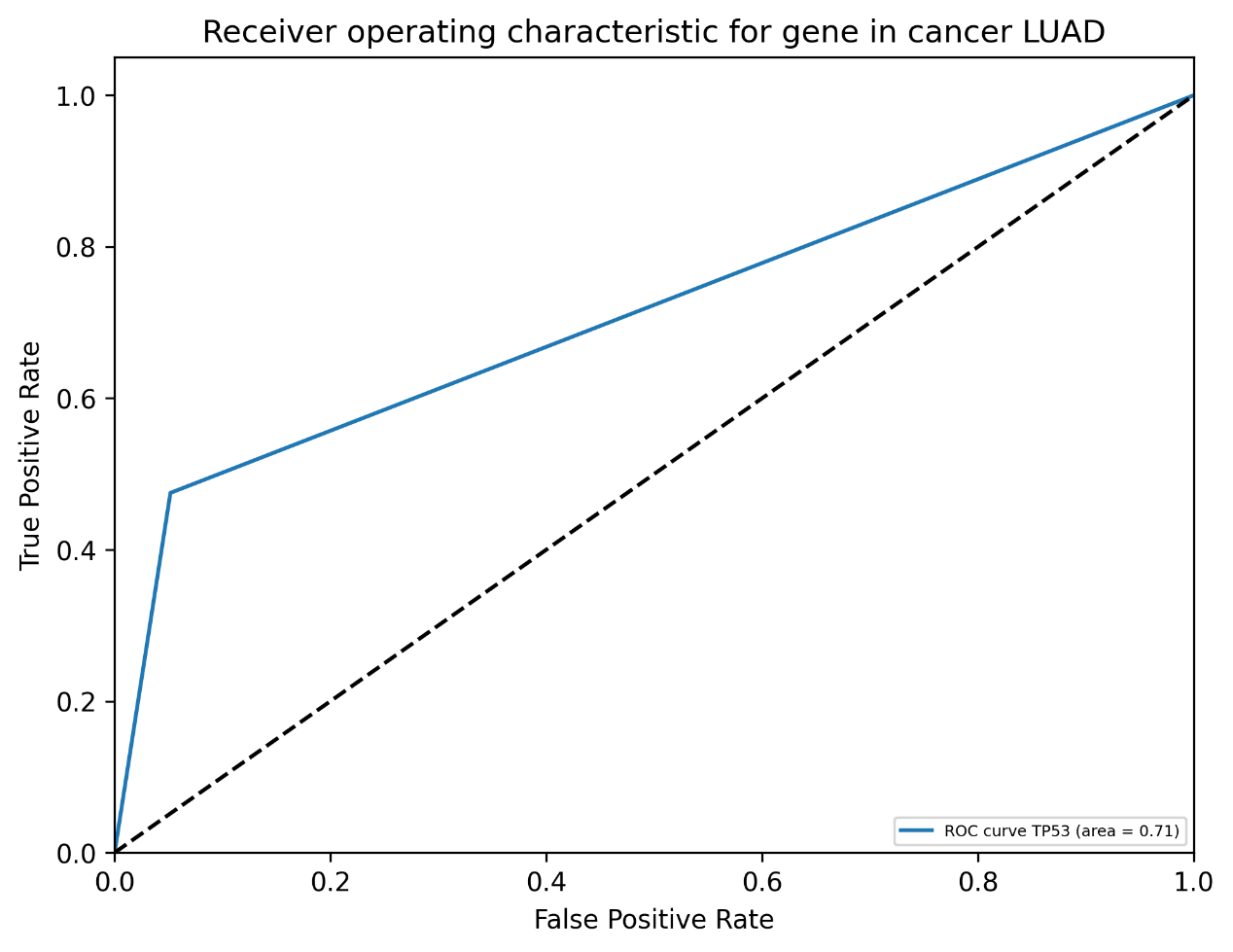
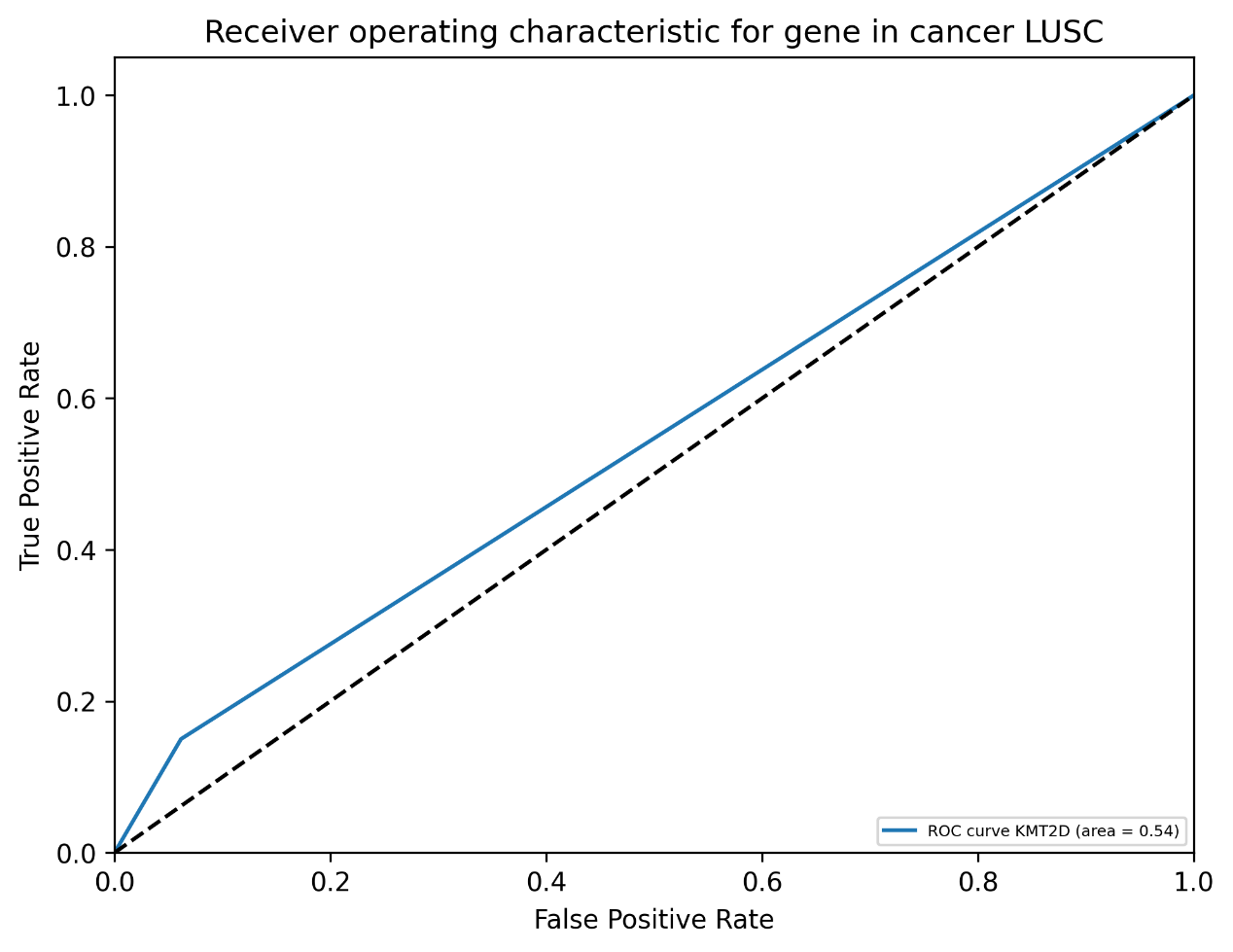
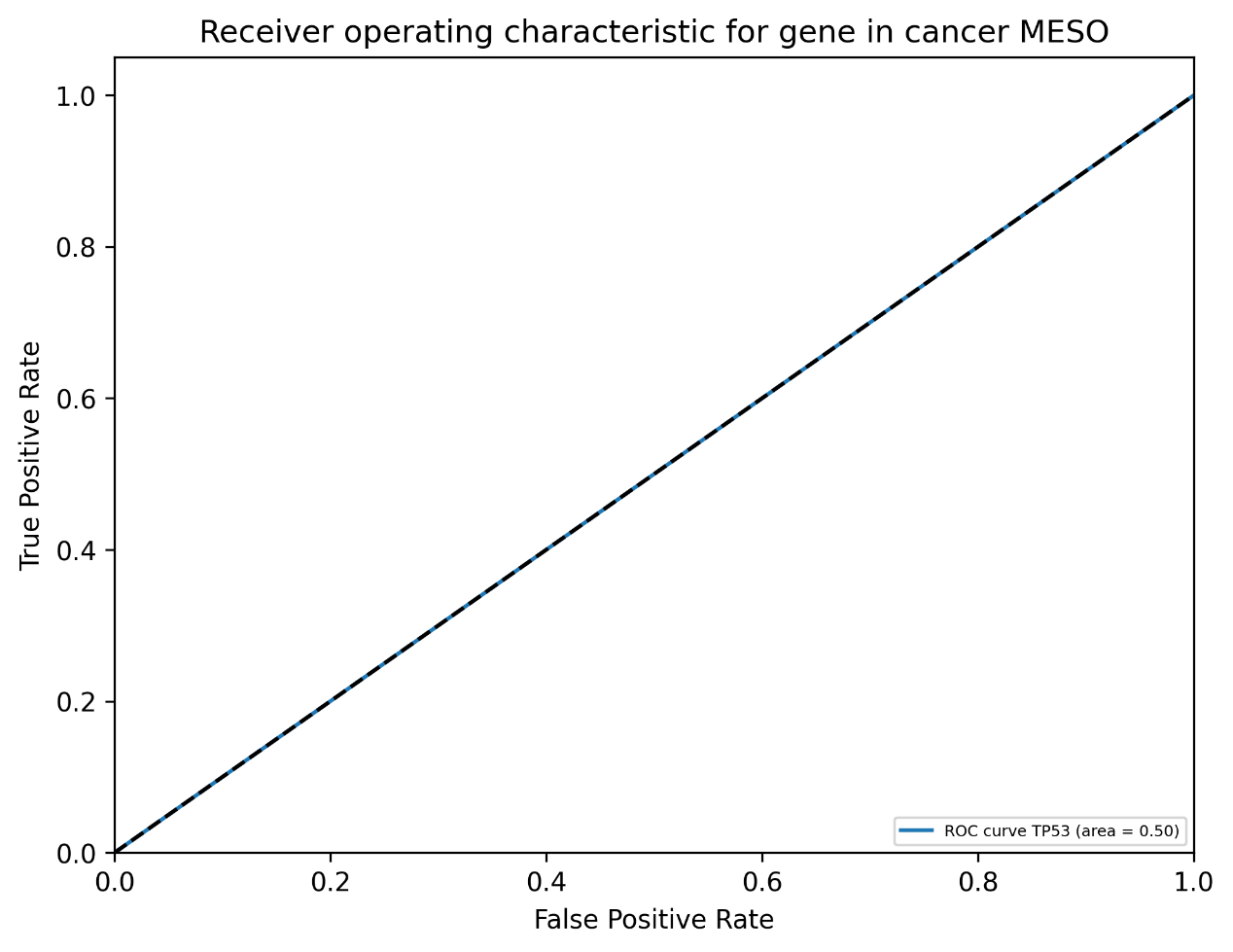
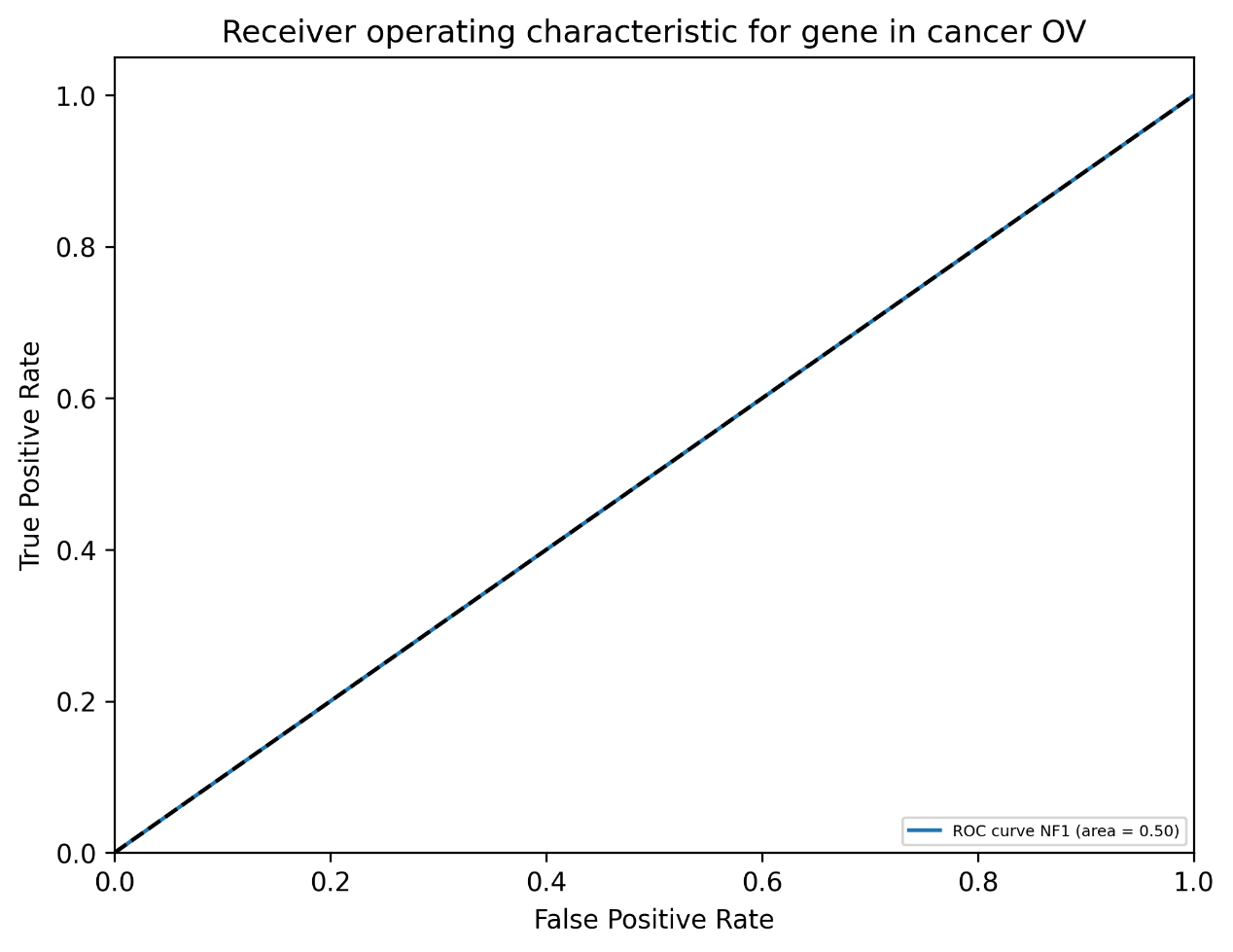
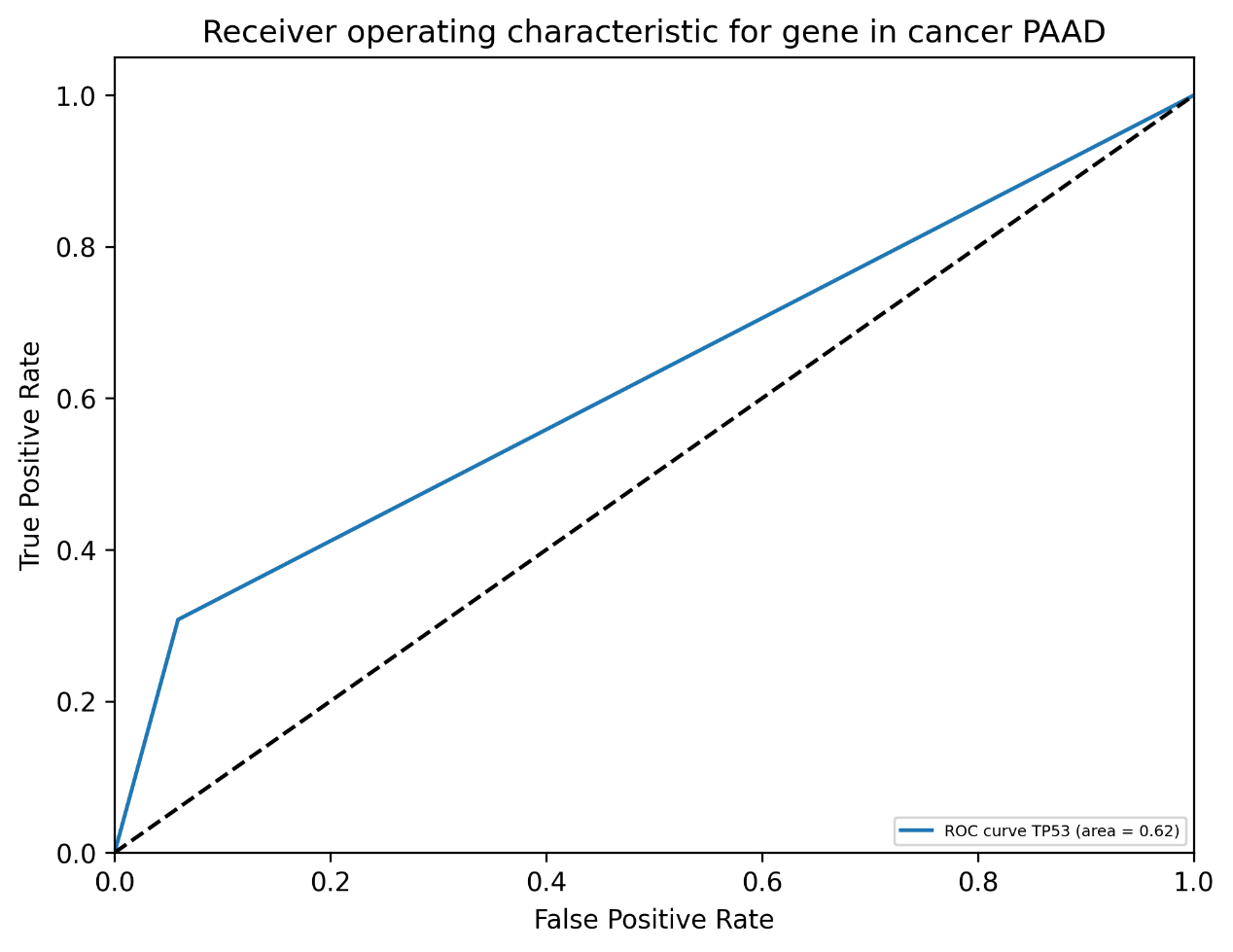
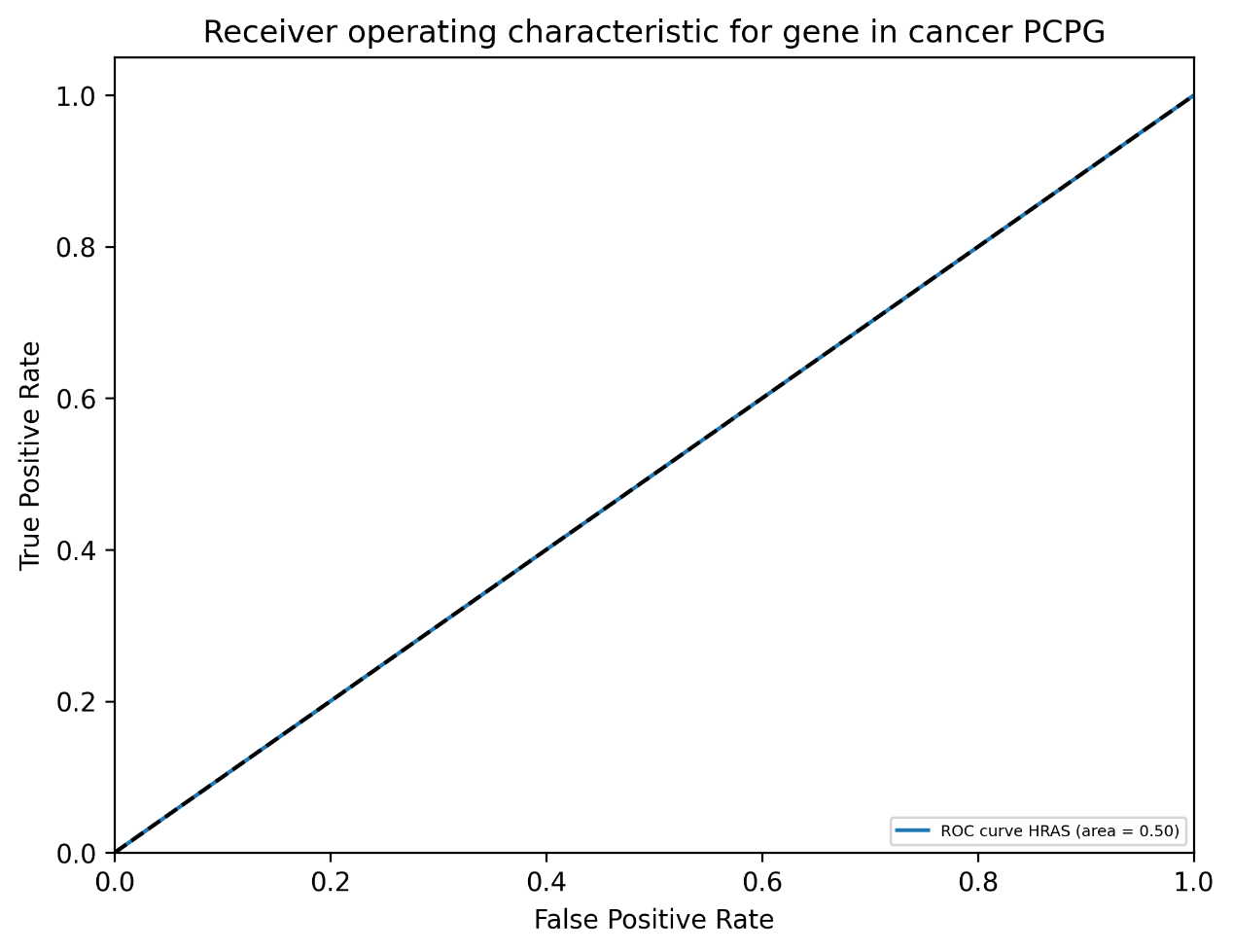
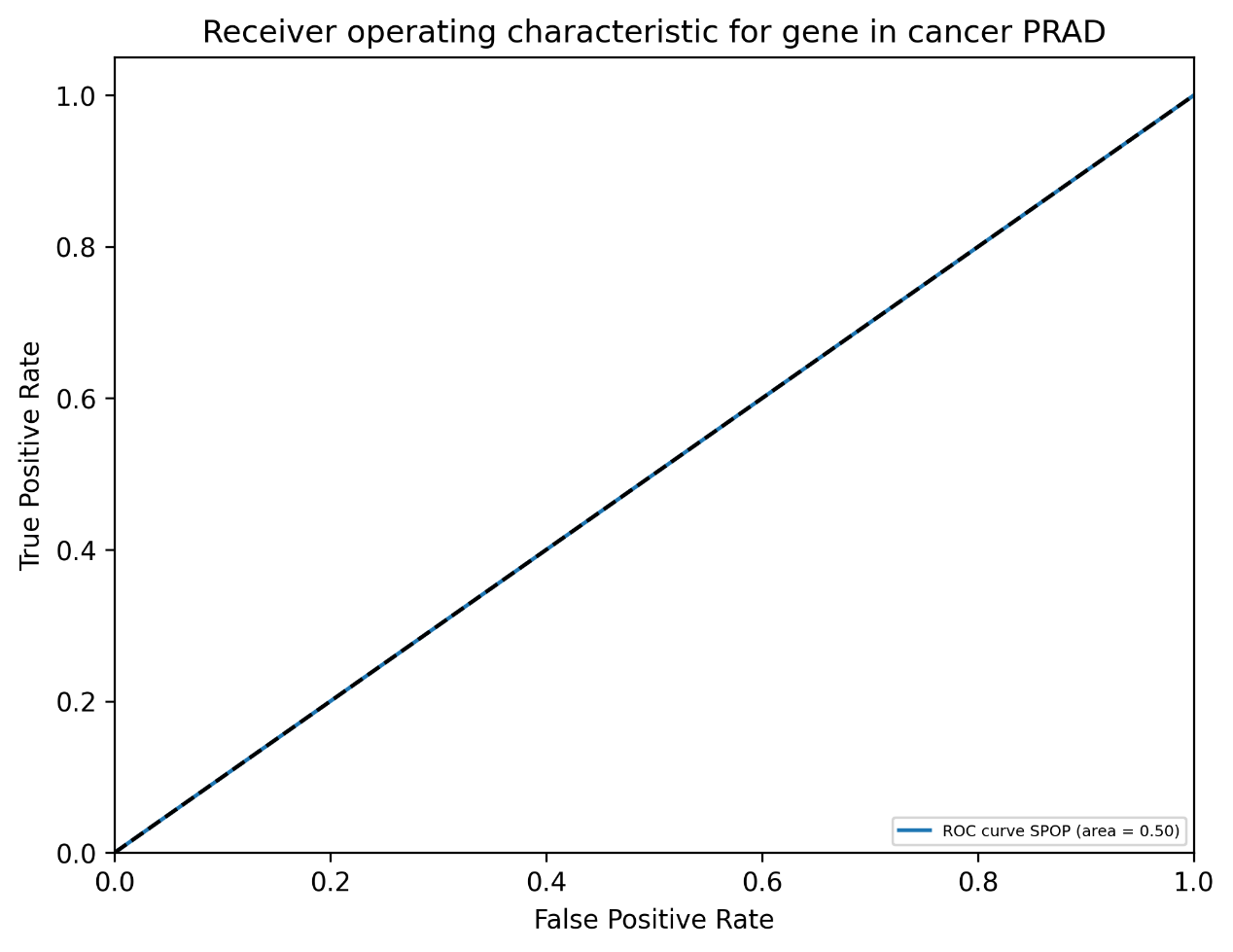
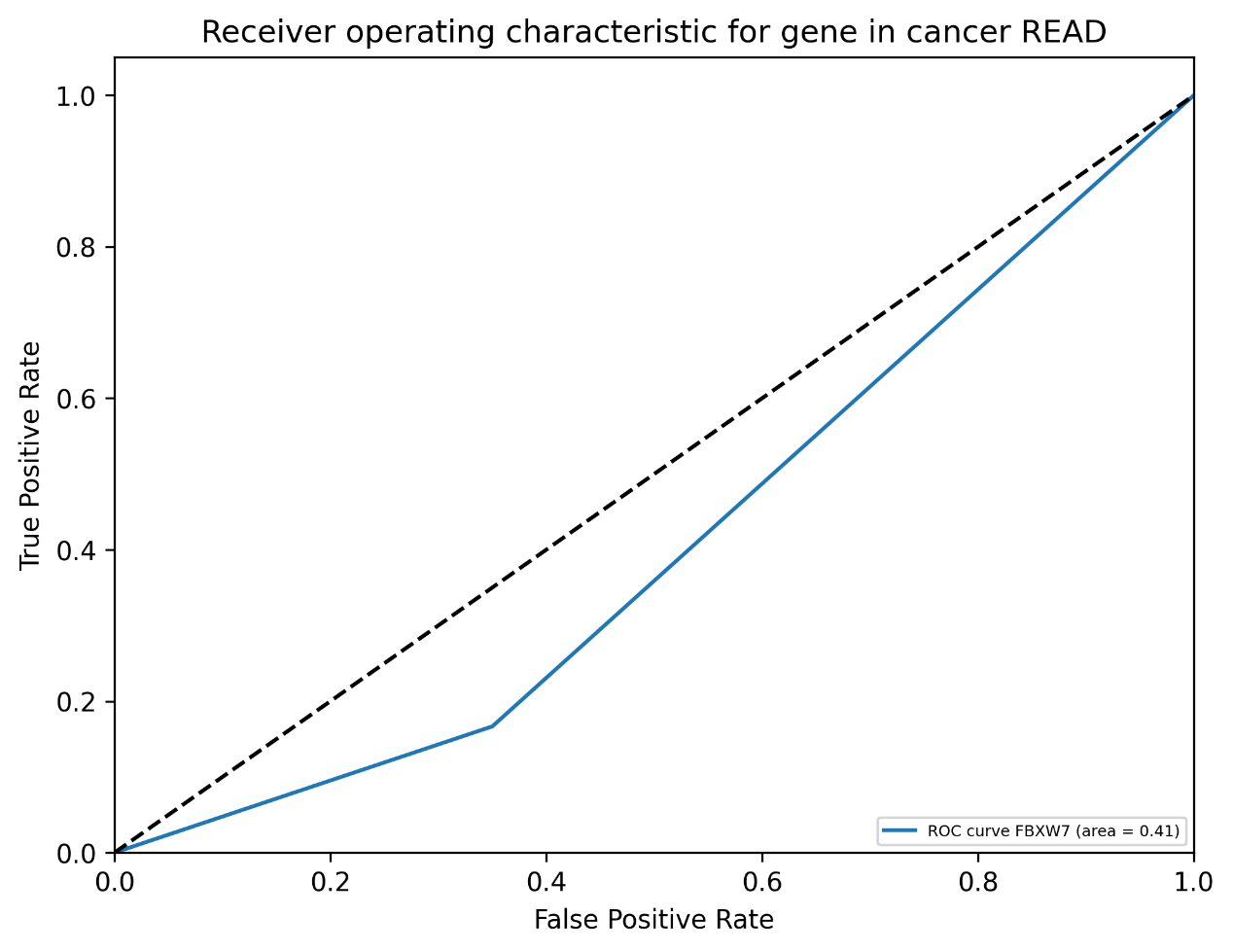
1. **What I have done:**

**(1).**

I used extracted sbs signatures to classify on the gene mutation status, the performance is also not good.

Later, to deal with the fake high accuracy caused by severe class imbalance. I find the set of most frequently mutated driver gene in each cancer and extracted one gene that has the mutation frequency around 0.4-0.5 to minimize the occurrence of the class imbalance. However, the classification result is still negative.





Thus, I presume that in the later future, we could try more data and perhaps try different mutational signatures as feature to see if we could obtain some positive result from it, but, at moment, we find that it is hard to build a recommender system to precisely predict on the patient’s gene mutation status.

**(2).**

I finished automatic running for the project so that we can run all the experiment with single command.

**(3).**

Wrote some part in dissertation.

1. **The problems:**
2. could you give me some insight in what I have written in dissertation?

**3.The plan**

(3). working on the dissertation